5.1.7	Biocceleration Ltd.
version	- 2006
GenCore	(c) 1993
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OM nucleic - nucleic search, using sw model

March 4, 2006, 01:46:27; Search time 2053.47 Seconds (without alignments) 295.138 Million cell updates/sec Run on:

US-09-701-583A-9 18 1 cggcatgtctatttgta 18 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

41078325 segs, 23393541228 residues

Searched:

106998 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST: * Database :

9b est1: *
9b est2: *
9b best2: *
9b best4: *
9b est6: *
9b est6: *
9b est6: *
9b est7: *
9b gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AZ84667 2M0146P24	AU258674 AU258674	BZ287861 SALK 0212	AZ822722 2M0096008	CL313440 mth2-128N	CZ469644 c04964-5p	CZ477101 d10098-3p	AB081925 Drosophil	CZ487985 f05420-3p	AZ402083 1M0169A15	AZ471813 1M0286D06	'AG192945 Pan trogl	CA851372 D13A08 A0	AJ587601 Arabidops	BZ768666 SALK 1405	AI690628 tx98g09.x	CZ470021 C05477b-5	AV852639 AV852639	CZ489987 f07187-5p	AU006827 AU006827	AZ478637 1M0298B23	AZ803680 2M0064009
ID	AZ846667	AU258674	BZ287861	AZ822722	CL313440	CZ469644	CZ477101	AB081925	CZ487985	AZ402083	AZ471813	AG192945	CA851372	AJ587601	BZ768666	A1690628	CZ470021	AV852639	CZ489987	AU006827	AZ478637	AZ803680
DB	9	н	σ	6	10	10	10	10	10	6	σ	10	9	10	σ		70	7	10	-	6	6
* Query · Match Length DB	24	34	37	40	20	30	37	29	30	21	28	31	36	24	27	28	30	34	37	. 39	27	53
% Query Match	6.89	68.8	68.8	68.8	65.6	65.6	9:59	64.4	64.4	63.3	63.3	63.3	63.3	62.2	62.2	62.2	62.2	62.2	61.1	61.1	0.09	60.0
Score	12.4	12.4	12.4	12.4	11.8	11.8	11.8	11.6	11.6	11.4	11.4	11.4	11.4	11.2	11.2	11.2	11.2	11.2	11	11	10.8	10.8
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AU009970 AU009970 AU009989 AU009989 BX532321 Arabidops BX532876 Arabidops	CA811642 D16A01 B1 AV836794 AV836794 D11586 HUMO012H05 D11855 HUMHMO2G12	N30120 yw63h05.81 BX661869 Arabidops AZ38982 1M0164D08	AZ76724 IMDS66E15 CZ551808 CB2_1687 CZ919151 4021012A0 AL944589 Arabidops	A1016852 ou27b03.x AL944588 Arabidops CZ559623 PL00353-5 BX536158 Arabidops	A2768574 IMO559P01 A2768828 IMO569C06 C2467409 c01749-3p C2483624 f01137-3p
AU009970 AU009989 BX532321 BX532876	CA851642 AV836794 D11586 D11855	N30120 BX661869 AZ398982	AZ767524 CZ551808 CZ919151 AL944589	A1016852 AL944588 CZ559623 BX536158	AZ763574 AZ768828 CZ467409 CZ483624
	9 11 8 8	8 0 6	6255	-999	999
31 31 31	8 8 8 8 8 8 8 4	W W W I	3 3 9 8	37 38 40	25 25 25 25
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10.8 10.8 10.8	10.8 10.8 10.8	10.8	10.8 10.8 10.8	10.8 10.8 10.8	10.6
223 254 265	30 30 30	33	35 36 37	38 39 41	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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ALIGNMENTS

RESULT 1

A284667	
LOCUS	A2846667 321-FEB-2001
DEFINITION	2M0146P24R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
.*	clone UUGC2M0146P24 R, genomic survey sequence.
ACCESSION	AZ846667
VERSION	AZ846667.1 GI:13027929
KEYWORDS	
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
REFERENCE	1 (bases 1 to 24)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
	Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
	Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
	Niederhausern, A. and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
	plasmid inserts
JOURNAL	
COMMENT	
	University of Utah Genome Center
	y of Utah
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
	84112, USA
	Tel: 801 585 5606
	Fax: 801 585 7177
	Email: ddunn@qenetics.utah.edu
	Insert Length: 10000 Std Error: 0.00
	Plate: 0146 row: P column: 24
	Seq primer: CACACAGGAAACAGCTATGACC
•	Class: plasmid ends
	High quality sequence stop: 24.
FEATURES	Location/Qualifiers
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	/organism="Mus musculus"
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	/sex="Male"
	/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
	/clone_lib="Mouse_lokb plasmid_UGCIM_library" /wote="Westor: bund2mm; Durified genomic_hub_from M
	/ HOCK - VECTOI: FRUITING GENOMIC DAY FLOM H.

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BZ287861 37 bp DNA linear GSS 24-OCT-2002 SALK 021239.53.05.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_021239.53.05.x, genomic
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2M0096C08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0096C08 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

[ (bases 1 to 37)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Alonso,C., Jeske,A., Rarnes,M., Ranco,M., Ranco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3702"
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/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (Sase 1 to 40)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At1908980.
Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.9%; Score 12.4; DB 9; Length 37; ilarity 92.9%; Pred. No. 1.8e+05; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 490 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GCATGTCTATTTTG 16
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                                                                                                                                                                                       survey sequence.
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                                                                            LOCUS
                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
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                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
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COMMENT
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AZ822722
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                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwaled [10] A732114[9] A722072.1], a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chamically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 34)

Kato, K. and Matoba, R.

Generation of expressed sequence tags from mouse brain Unpublished (2002)

Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

8916-5 Takayama, Ikoma, Nara 630-0101, Japan
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BED0013458 3', mRNA sequence.
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AU258674.1 GI:20324462
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Matches 13; Conserv
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ORGANISM
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ACCESSION VERSION

KEYWORDS

RESULT 2 AU258674

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AUTHORS TITLE JOURNAL COMMENT

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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Robera; Brdopterygota; Diptera; Brachycera; Muscomorpha;

Ropera; Drosophildae; Drosophila.

El (bases 1 to 30)

El (bases 1 to 30)

El Thbault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Singh, C.M., Antouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Iaufer, A., Mazzotta, J., Smith, R.D., Stevens L.M., Stuber, C., Iaufer, A., Mozyanski, C., Swimmer, C., Kopczynski, C., Duvk, G., Winberg, M. L. and Margolis, J. Swimmer, C., Kopczynski, C., Duvk, G., Winberg, M. L. and Margolis, J. A complementary transposon tool kit for Drosophila melanogaster
Jakab, J., Deak, G., Kevei, Z., Karchesz, K., Sarai, E., Kiss, P.,
Kereszt, A., Kalo, P., Endre, G. and Kiss, G.B.
Medicago Truncatula BAC end sequencing
Unpublished (1204)
Contact: Deak, G.
Alfalfa Genomics Group; Medicago Genetics Group
Agricultural Biotechnology Center; Biological Research Center
P.O. Box 411, Hungary, H-2100 Godollo, Szent-Gyorgyi Albert ut 4.;
P.O. BOX 521, Hungary, H-6701 Szeged, Temesvari krt. 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:3880"
/sex="Hermaphrodite"
/clone_lib="Medicago truncatula BAC end sequences"
/clone_lib="Medicago truncatula BAC end sequences"
/note="Torgan: Leaf; Vector: pBelol1; Site 1: HindIII;
Site_2: HindIII; Construction of a bacterial artificial
chromosome library of Medicago truncatula and
identification of clones containing ethylene-response
genes. Theor Appl Genet (1999) 98: 638-646 Y.-W.,Nam;
R.V.,Penmetsa; G.,Endre; P.,Uribe; D.,Kim; D.R.,Cook"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CZ469644 100 30 bp DNA linear GSS 29-APR-2 c04964-5prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 5' end of piggyBac,
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Lawrence Berkeley National Laboratory
Mailbrop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.6%; Score 11.8; DB 10;
81.2%; Pred. No. 3.6e+05;
ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="Jemalong"
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Nat. Genet. 36 (3), 283-287 (2004)
14981521
                                                                                                                                                                                                                                                                                                               Fax: 3628526193
Email: gdeak@abc.hu
Plate: 128 row: N column: 01
Seq primer: OP Reverse
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence.
CZ469644
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Best Local Similarity 81.24
Matches 13; Conservative
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CZ469644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwapto. [4] 4732114[gb]AR129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 01-MAR-2004
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGCIM library"
//note="Vector: PMP42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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mth2-128N01_OP Medicago truncatula BAC end sequences Medicago
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                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 10000 Std Brror: 0.00 Plate: 0096 Trw: O column: 08 Seq primer: CGTTGTAAAACGACGCCAGT Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10090"
clone="UUGC2M0096008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 40.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Matches 13; Conserv
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84112, US
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Query Match

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Brosophila melanogaster

Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Bobydroidea; Drosophilidae; Brosophila.

Ephydroidea; Drosophilidae; Drosophila.

I (bases I to 37)

Thibalt, S. T., Singer, M. A., Miyazaki, W. Y., Milash, B., Dompe, N. A., Singh, C. M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H. L., Ryner, L., Cheung, L. M., Chong, A., Erickson, C., Fisher, W. M., Greer, K., Hartouni, S. R., Howke, B., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R. D., Stevens, L. M., Stuber, C., Tan, L. R., Ventura, R., Woo, A., Zakrajeek, I., Zaho, L., Chen, F., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M. L. and Margolis, J. A. Complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                   /db xref="taxon:722"
/db xref="taxon:722"
/clone llb="Exelixis piggyBac PB insertions"
/clone llb="Exelixis piggyBac PB insertions"
/clone llb="Exelixis piggyBac PB insertions"
/note="vector: piggyBac PB (GenBank accession number AY15146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilizated the PB element using the remobilization of transposable expression by immersing bottles in a circulating 370c water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic gequence by inverse PCR."
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                                                                The piggyBac insertion position is 27 in the 30 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence. Class: transposon insertion site.
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mallstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
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Pred. No. 3.6e+05;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                     organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/Btrain="isogenic w- strain"
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Nat. Genet. 36 (3), 283-287 (2004)
                                                                                                                                                          transposon insertion site.
Location/Qualifiers
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13; Conservative
                                                        piggyBac element.
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mobilized ammunition element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinscy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
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                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"

Strain="isogenic w- strain"

/db xref="taxon:7227"

/clone_lib="Exelixis P element XP insertions"

/note="Vector: P element XP (GenBank accession number

AX515149); An isogenic w- brosophila melanogaster strain

was mutagenized by remobilization of transposable
                                                                                                                              The P element insertion position is 1 in the 37 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
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Frederick; 1050 Boyles st., Frederick, Maryland 21702-1201, USA
(E-mail:ohsuwan@mail.ncifcrf.gov, Tel:1-301-846-7314,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB081925 25-FEB-2
Drosophila melanogaster DNA, clone:1(2)SH2 0218, genomic survey
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A p-element insertion screen identified mutations in 455 novel
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                  Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oh,S., Kingsley,T., Shin,H., Zheng,Z., Chen,H. and Hou,S. Direct Submission
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    organism="Drosophila melanogaster"

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86.7%; Pred. No. 3.6e+05;
live 0; Mismatches 2;
                               Sequence recovery method was inverse PCR.
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/db_xref="taxon:7227"
/clone="1(2)SH2 0218"
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Genetics 163 (1), 195-201 (2003)
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Email: RHoskins@lbl.gov
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Gaps

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Indels

Pred. No. 4.5e+05;

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Best Local Similarity 77.8%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L., Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W., Karner,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,R., Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C., Tan,L.R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F., Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L., and Margolis,J. A complementary transposon tool kit for Drosophila melanogaster
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/clone lib="Exelixis piggyBac WH insertions"
/clone lib="Exelixis piggyBac WH insertions"
/clone lib="Exelixis piggyBac WH (GenBank accession number
AY515148); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the WH element using the
constitutive alpha-1 tubulin:piggyBac transposase source.
We remobilized the WH element from a single ammunition
element on the Binsinscy balancer chromosome in dysgenic
                                                                                                                                                                                                                                                                                                              CZ487985 30 bp DNA linear GSS 29-APR-2 f05420-3prime Exelixis piggyBac WH insertions Drosophila melanogaster genomic Sequence recovered from 3' end of piggyBac,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of piggybac element.
The piggybac insertion position is 1 in the 30 bases. This insertion position refers to the first base of the 4 base TTAA
                                                                                   Gapa
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Drosophila melanogaster
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berkeley DrőBophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHOBKinB@lbl.gov
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                             Length 29;
                                                                                4; Indels
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"mol type="genomic DNA"
'strain="isogenic w- strain"
                          Score 11.6; DB 10;
Pred. No. 4.5e+05;
0; Mismatches 4;
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Nat. Genet. 36 (3), 283-287 (2004)
14981521
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Class: transposon insertion site.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence.
CZ487985
                                                                                                                                   1 CGGCATGTCTATTTTGTA 18
                                                                                                                                                              29 CAGCAGGTCTAATTTGAA 12
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                             64.4%;
ilarity 77.8%;
Conservative
                                                     Similarity
                             Query Match
Best Local Simi
Matches 14;
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KEYWORDS
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3 4 4

64.4%; Score 11.6; DB 10; Length 30;

Query Match

ORIGIN

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfa732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                           AZ402083 21 bp DNA linear GSS 03-0CT-2000 1M0169A1SF Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0169A15 F, genomic survey sequence.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone_lib="Mouse_10kb plasmid UUGCNH library"
/note="Vector: PWDAny, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 21)
Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0169 row: A column: 15
Seq primer: cGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0169A15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
1 CGGCATGTCTATTTTGTA 18
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                                                                        19 cecrrrrrrrrrrrrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
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Fax: 801 585 7177
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63.3%; Score 11.4; DB 9; Length 28; 92.3%; Pred. No. 5.7e+05; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-069M06.T7"
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R.Site 1 : EcoRI
R.Site 2 : EcoRI
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GSS.
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                       Query Match 63.3'
Best Local Similarity 92.3'
Matches 12; Conservative
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                          sequence.
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CA851372/c
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacree, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Nouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
University of Utah Genome Center
University of Utah
Sweise Robert B. Weiss
                                                                                                                                                                                                                                                                         AZ471813 28 bp DNA linear GSS 04-OCT-2000 IM0286D06R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0286D06 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sclurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_llb="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G79BL/G0 (male) was obtained from the Jackson
                                                    Gaps
                                                    ö
63.3%; Score 11.4; DB 9; Length 21; 92.3%; Pred. No. 5.7e+05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0266 row: D column: 06
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
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organism="Mus musculus"
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'strain="C57BL/6J"
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/clone="UUGC1M0286D06"
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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                                                                                                   3 GCATGTCTATTTT 15
                                              12; Conservative
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                          Similarity
  Query Match
                          Best Local
Matches 1
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AZ471813/c
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TITLE

COMMENT

ORIGIN

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36 bp mRNA linear EST 01-AUG-2003 D13A08 A08_02.abl cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D13A08 5', mRNA sequence.
CA851372 GR851372.1 GI:33388165
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(bases 1 to 31)

Park, H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,

Park,H., Kim,Y., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.

Direct Submission

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);

S.2, Oun-dong, Yusong-qu, Daejeon 305-333, Korea

(E-mail:redstone@mail:kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,

Tel:82-42-866-7181, Fax:82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: RP43-069M06.T7, genomic survey
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Gaps
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/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
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survey sequence.
BZ768666
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Best Local Similarity
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BZ768666/c
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                                                                                                                                 To Topics 1 to 36)
Alkharouf,N., Khan,R. and Matthews,B.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Genome 47 (2), 380-388 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana T-DNA flanking sequence, left border, clone 298H08, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment (s) resulting from the PCR were directly sequenced from the left or the right border
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T-DNA integration into the Arabidopais genome depends on sequences
                                                                                                                                                                                                                                                          Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Roots"
/dev stage="Seedlings"
/clome_tib="coma Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
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GSS; left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Pred. No. 5.8e+05;
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EMBO Rep. 3 (12), 1152-1157 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                   Email: alkharon@ba.ars.usda.gov
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "mol_type="mRNA"
'cultivar="Peking"
'db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="D13A08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.3%;
80.0%;
  EST.
Glycine max (soybean)
Glycine max
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                                                                                                                                                                                                                                                                                                                                                            Tel: 301 504 5750
Fax: 301 504 5728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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KEYWORDS
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AUTHORS
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 27)
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A Sequence-Indexed Library of Insertion Mutations in the
to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and 'http://genoplante.info.infoblogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at
                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BZ768666 SALK 140548.46.70.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_140548.46.70.x, genomic
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/clone="SALK 140548.46.70.x"
/clone=lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οţ
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.2%; Score 11.2; DB 10;
ilarity 81.2%; Pred. No. 7.2e+05;
Conservative 0; Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
|mol_type="genomic DNA"
|AD_xref="taxon:3702"
|clone="298H08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .24
/note="T-DNA flanking sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /ecotype="Wassilewskija"
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/ecotype="Col-0"
                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGCGTGTGTAATTTGT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       left border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGCATGTCTATTTGT
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the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

ö 0; Gaps Query Match
Best Local Similarity 81.2%; Pred. No. 7.2e+05;
Matches 13; Conservative 0; Mismatches 3; Indels

g ò

Search completed: March 4, 2006, 03:39:01 Job time : 2857.47 secs

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Sequence 243, App
Sequence 91037, A
Sequence 121656,
Sequence 121866,
Sequence 259860,
Sequence 259860,
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Sequence 474175,
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                                                                                                                     March 4, 2006, 01:49:48; Search time 375.632 Seconds (without alignments) 396.263 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40, 1
Sequence 185, Sequence 529, Sequence 116,
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Sequence 197,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications_NA_Main:*

1: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-189-267-185
US-10-984-919-529
US-10-189-267-116
US-10-189-267-213
US-10-098-263B-91037
US-11-036-317-121656
US-11-060-756-1290386
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US-11-036-317-253543
US-11-036-317-276997
US-11-036-317-310713
US-11-036-317-334637
US-11-036-317-383155
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                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                  9793542 segs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                 nucleic search, using sw model
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18
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               Copyright
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Match 1
                                                                                                                                                                                                             Title:
Perfect score:
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                                                                                                                                                                                                                                                          Sequence:
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Seguence 777184, Seguence 180828,	Sequence 583979,	Sequence 715769,	Seguence 198172,	Sequence 229607,	Sequence 239950,	Sequence 294363,	Sequence 322759,	Sequence 439359,	Sequence 7, Appli	Sequence 55957, A	Seguence 518120,	Sequence 60048, A	Sequence 589217,	Sequence 592572,	Seguence 808618,	Sequence 51384, A	Sequence 51387, A	Sequence 51389, A	Sequence 51390, A	Sequence 271471,
US-11-036-317-777184 US-10-719-956-180828	US-10-719-956-583979	US-10-719-900-715769	US-11-036-317-198172	US-11-036-317-229607	US-11-036-317-239950	US-11-036-317-294363	US-11-036-317-322759	US-11-036-317-439359	US-10-053-662A-7	US-10-098-263B-55957	US-10-719-956-518120	US-10-719-900-60048	US-10-719-900-589217	US-10-719-900-592572	US-10-719-900-808618	US-10-956-157-51384	US-10-956-157-51387	US-10-956-157-51389	US-10-956-157-51390	US-10-956-157-271471
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14 77.8 13.8 76.7	13.8 76.7	13.8 76.7	13.8 76.7	13.8 76.7	13.8 76.7	13.8 76.7	13.8 76.7	13.8 76.7	13.4 74.4	13.4 74.4	13.4 74.4	13.4 74.4	13.4 74.4	13.4 74.4	13.4 74.4	13.4 74.4	13.4 74.4	13.4 74.4	13.4 74.4	13.4 74.4
C 24	c 26	C 27	28	29	30	31	32	c 33	34	. 35	c 36	37	38	39	40	41	42	43	44	45

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transforming-growth-factor beta
                                                                                                                                                                                              APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth
NUMBER OF SEQUENCES: 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Jacobson, Price, Holman & Stern
400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRICATION DATA:
PRICATION UNMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-WAY-1993
ATTORNEY/AGENT INFORMATION:
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELEPOMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                        Sequence 72, Application US/10146058 Publication No. US20030040499A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/535,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 72.
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CITY: Washington D.C
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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ZIP: 20004
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FEATURE:
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; Sequence 1209, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INPORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Karl-Hermann
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P637631080
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1999-0-24
; PRIOR FILING DATE: 1998-01-30
; PRIOR FILING DATE: 1998-01-30
; PRIOR FILING DATE: 1998-01-30
; RIOR RILING DATE: 1998-01-30
; RIOR SPLING DATE: 1998-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: antisense; OTHER INFORMATION: oligonucleotide
US-10-220-033-4
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                                                                                                                                                100.0%; Score 18; DB 5; Length 18; 100.0%; Pred. No. 35;
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                                                          unknown
E: DNA (genomic)
YES
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             LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 18; Conservative
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Matches 18, Conservative
SEQUENCE CHARACTERISTICS
                           TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: unkn
MOLECULE TYPE: D
ANTI-SENSE: YES
US-10-146-058-72
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; Sequence 40, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PO. 0.036
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284
; SEQ ID NO 40
; LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1277, Application US/1094919
; Sequence 1277, Application US/1094919
; Publication Wo. US20050130927A1
; Generation Wo. US20050130927A1
; Generation Wo. US20050130927A1
; Generation Wo. US20050130927A1
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE PREPARATION METHOD
; FILE REPERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT APPLICATION NUMBER: US/09/311,700
; PRIOR APPLICATION NUMBER: PP 974
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1998-01-30
; PRIOR FILING DATE: 1997-01-31
; RRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 16
; TYPE: DNA
CURRENT: Artificial Sequence
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                                                                                                                                                                                                                               9; Length 18;
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                                                                                                                        ) OTHER INFORMATION: Description of Artificial Sequence:

) OTHER INFORMATION: antisense oligonucleotide

US-10-984-919-1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1277
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88.9%; Score 16; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                            Score 18;
Pred. No. 3
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                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative 0
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SEQ ID NO 1209
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 243, Application US/10189267
Publication No. US20040006030A1
GENERAL INFORMATION:
                                                                                                                                                                            Sequence 116, Application US/10189267
Publication No. US20040006030A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
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                                                            1 dcargreraririgia 16
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Best Local Similarity 88.9
Matches 16; Conservative
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: M. musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-10-098-263B-91037
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                                                                                                                                                         JS-10-189-267-116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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APPLICANT: Sugan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
FILE REPERBICE: PTS-0038
CURRENT APPLICATION NUMBER: US/10/189,267
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 284
LENGTH: 20
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APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Brysch, Wolfgang
TILLE OF INTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
FILE REFERENCE: 10496/P63763USO
CURRENT APPLICATION NUMBER: US/10/984,919
                                                                                      88.9%; Score 16; DB 6; Length 20; 100.0%; Pred. No. 3.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.9%; Score 16; DB 6; Length 20; 100.0%; Pred. No. 3.7e+02; ive 0; Mismatches 0; Indels
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, OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-529
; FRATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-40
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PRIOR APPLICATION NUMBER: US/09/341,700

PRIOR FILING DATE: 1999-09-24

PRIOR FILING DATE: 1999-09-24

PRIOR FILING DATE: 1998-01-30

PRIOR PILING DATE: 1998-01-30

PRIOR PILING DATE: 1997-01-31

NUMBER OF SEQ ID NOS: 1764

SOFTWARE: Patentin Ver: 2.1

LENGTH: 20
                                                                                                                                                                                                                                                                                                                        Sequence 185, Application US/10189267
Publication No. US20040006030A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
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Publication No. US20050130927A1
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                                                                                   Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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ORGANISM: H. sapiens
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APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Schneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
FILE REPREBRUCE: PTS-0038
CURRENT APPLICATION NUMBER: US/10/189,267
CURRENT APPLING DATE: 2002-07-02
SEQ ID NOS: 284
SEQ ID NO 116
LENGTH: 20
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APPLICANT: Susan M. Dobie
TILLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
FILE REPERRENCE: PTS-0038
CURRENT APPLICATION NUMBER: US/10/189,267
CURRENT APPLICATION DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 284
SEQ ID NO 243
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Sequence 259860, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
APPLICANT: Wounts, William Martin
APPLICANT: Mounts, William Martin
APPLICANT: NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin Version 3.2
LENGTH: 25
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Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
       Gaps
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; Sequence 865692, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
    APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 865692
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Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2;
         5
         Mismatches
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
       16; Conservative
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US-10-719-900-865692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: probe
US-11-060-756-259860
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       Matches
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| Sequence 190386, Application US/11060756
| Publication No. US20050221354A1
| GENERAL INFORMATION
| APPLICANT: Wyeth
| APPLICANT: Would: William Martin
| APPLICATION: Target Genes
| TITLE OF INVENTION: Target Genes
| FILE REFERENCE: AM101083 (031896-042000)
| CURRENT PILING DATE: 2005-02-18
| NUMBER OF SEQ ID NOS: 303284
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 190386
| LENGTH: 25
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| Publication No. US20050214823A1
| Publication No. US20050214823A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Alan
| APPLICANT: Blume, John
| TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
| TILLE REFERENCE: 3654.1
| CURRENT PILIAN DATE: 2005-01-13
| PRIOR APPLICATION NUMBER: US 60/536,639
| PRIOR APPLICATION NUMBER: US 60/536,639
| PRIOR PILING DATE: 2004-01-13
| NUMBER OF SEQ ID NOS: 991174
| SEQ ID NO 121656
| LENGTH: 25
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                                                                                                                                                                                                                                                                                          Score 14.8; DB 5; Length 25; Pred. No. 1.5e+03;
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 91037
LENGTH: 25
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Pred. No. 1.5e+03;
0; Mismatches 2
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                 ORGANISM: Homo sapien
US-10-098-263B-91037
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Best Local Similarity
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; ORGANISM: probe
US-11-060-756-190386
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; FILE REPERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SEQ ID NO 194446
; SEQ ID NO 194446
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; ORGANISM: Mus musculus
US-11-036-317-194446

Query Match
Best Local Similarity 93.8%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0

Qy 3 GCATGTCTATTTGTA 18

Qy 3 GCATGTCTATTTGTA 18

Db 25 GCATGTCTATTTGTA 10
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Search completed: March 4, 2006, 07:04:14 Job time : 375.632 secs

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US-11-121-849-319625

Sequence 319625, Application US/11121849

Sequence 319625, Application NS/11121849

Sequence 319625, Application NS US20050272080A1

GENERAL INFORMATION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR FILING DATE: 2004-05-03

PRIOR FILING DATE: 2004-05-03
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Matches 17; Conservative 0;
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Sequence 319625,
Sequence 461071,
Sequence 378741,
Sequence 1375953,
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Sequence 153306,
Sequence 153312,
Sequence 153313,
Sequence 153325,
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Sequence 153341,
Sequence 245961,
Sequence 1437211
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                                                                                                                     March 4, 2006, 01:58:42; Search time 446.211 Seconds (without alignments) 88.444 Million cell updates/sec
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Sequence 1
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1: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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/cgn2 6/prodata/1/pubpna/US11_NEW_PUB.seq3:*
/cgn2 6/prodata/1/pubpna/US11_NEW_PUB.seq4:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-121-849-151115

2 US-11-136-527-153312

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2 US-11-101-244-1437211

US-11-011-244-1437212

US-11-01-244-1437212

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Maximum Match 100%
Listing first 45 summaries
                                                                                - nucleic search, using sw model
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Perfect score:
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	•	23	_	72.2	25	17	US-11-121-849-108655	
	טנ	4 C	12.8	71.1	B 6	10 CC	US-10-310-914A-291549 IIS-10-310-914A-1023769	Sequence 291549, Sequence 1023769.
	,	56	12.8	71.1	13	10	US-11-101-244-617220	Sequence 617220,
•		27	12.8	71.1	19	10	US-11-101-244-617251	
		28	12.8	71.1	13	10	US-11-101-244-1125173	Sequence 1125173,
		۶ ر د	12.8	71.1	y (7 =	US-11-063-784-617220 US-11-083-784-617251	Sequence 617250,
		31	12.8	71.1	13	17	US-1:1-083-784-1125173	
	υ	32	12.8	71.1	20	6 0	US-10-310-914A-375180	Sequence 375180,
	U	33	12.8	71.1	21	80	US-10-310-914A-289791	
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	O	37	12.8	71.1	23	ω	US-10-310-914A-375181	
	υ	38	12.8	71.1	23	œ	US-10-310-914A-805246	
	υ	39	12.8	71.1	23	œ	US-10-310-914A-1023780	
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		7 7	12.0	7.1.1	0 0	, a	US-IU-SIU-VI4A-564999 IIC-11-121-646-2242	Sequence 364999,
		7 4	12.0	71.1	n i	7 5	0	
		ֆ 4	12.8	71.1	2 C	7 5	-121-849-1128 -121-849-1507	Sequence 112895,
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							ALIGNMENTS	
	RES	RESULT 1		,				
	us-	11-12	US-11-121-849-319164	19164				
		ednen	ce 31910	64, Appli	catio	n US	Sequence 319164, Application US/11121849	
	Ω,	ublic	ation No	Publication No. US20050272080A1	502720	80A1		
		ENERA	GENERAL INFORMATION:	MATION:				
		APPLI	CANT: J	APPLICANT: John Palma				
	٠.	TITLE	OF INV	ENTION: N	echod	s of	enetic Analysis of	Formalin Fixed Paraffin Embedded S
		TITLE	OF INV	TITLE OF INVENTION:	Microarrays	arre	ıys	
		FILE	REFEREN	FILE REFERENCE: 3684.1	-	- 1	FILE REFERENCE: 3684.1	
	٠	CURRE	NT APPL	CURRENT APPLICATION NUMBER: US/1	NUMBER	 	5/11/121,849	
		CUKKE	INI FILLI	CORRENT FILING DAID: 2005-05-03	0007		03	
		PRIOR	PILING	PRIOR AFFELCATION NUMBER: 00/	104-05	700	0,100	
		NUMBE	R OF SE	NUMBER OF SEC ID NOS: 673904	6239	9 6		
		SOFTW	ARE: Mi	croarray	Probe	Sec	SOFTWARE: Microarray Probe Sequence Listing Generator V	1.1
	co 	EQ ID	EQ ID NO 319164	164				
	. ••	LENGTH:	TH: 25					
	•	TYPE	TYPE: DNA					•
		ORGA	NISM: H	ORGANISM: Homo sapien	ue			
	us-	11-12	-11-121-849-319164	19164				
	0	Ouerv Match	Match		94	94.48;	Score 17; DB 12; Length	. 25;
•	Щ	est, L	ocal Sir	Best Local Similarity	100		Pred. No. 17;	
	Σ	Matches	в 17;	Conservative	vative		0; Mismatc	ls 0; Gaps 0;

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2 GGCATGTCTATTTG 16
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Matches 14; Conservative
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; ORGANISM: Homo sapien
US-11-121-849-151115
                                                                                   JS-10-310-914A-1375953/c
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Best Local Similarity
Matches 14; Conserv
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US-11-121-849-151115
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 461071, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Isaac
APPLICANT: Bentwich, Rvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-310-914A-378741/c

Sequence 378741, Application US/10310914A

Publication No. US20060003322A1

Sequence 378741, Application US/10310914A

Sequence 378741, Application US/10310914A

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Bentwich, Isaac

APPLICANT: Biller, Kvuzat

TITLE OF INVENTION: uses thereof

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT RILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 378741

LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.7%; Score 13.8; DB 8; Length 22; 47.1%; Pred. No. 8.5e+02; ive 7; Mismatches 2; Indels
                                                                                                                                                                                                         DB 12; Length 25; 17;
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 319625
LENGTH: 25
                                                                                                                                                                                                      94.4%; Score 17; DB 100.0%; Pred. No. 17; ive 0; Mismatches
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Conservative
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Best Zocal Similarity 100.
Matches 17; Conservative
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                                                                                                         TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-319625
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hes 8; Conserv
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nes 15; Conserv
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US-10-310-914A-461071
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US-10-310-914A-461071
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US-10-310-914A-378741
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Matches 15
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us-09-701-583a-9.sz40.rnpbn

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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AM.01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 153317
LENGTH: 25
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
TITLE OF INVENTION: US - 031896 - 041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-26
NUMBER OF PAPPICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 153325
LENGTH: 25
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                                             Length 25;
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                                             74.4%; Score 13.4; DB 12; 93.3%; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                    Sequence 153317, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 153325, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
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Best Local Similarity 93.34
Matches 14; Conservative
                                        Query Match
Best Local Similarity 93.3
Matches 14; Conservative
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Probe US-11-136-527-153325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial
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ORGANISM: Artificial
    US-11-136-527-153313
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PILING DATE: 2005-05-26

NUMBER OF SEC ID NOS: 362830

SOFTWARE: Patentin version 3.2

LENGTH: 25

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Publication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 031896-041000 (AM101086)
CURRENT PEPLING DATE: 2005-06-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION DATE: 2005-06-26
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Pred. No. 1.4e+03;
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Pred. No. 1.4e+03;
0; Mismatches 1
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PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 153306
LENGTH: 25
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SOFWARE: Patentin version 3.2
SEQ ID NO 153312
LENGTH: 25
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                                                                                                                                                                                                                                 74.48;
93.38;
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                                                                                                                                                                 OTHER INFORMATION: Probe US-11-136-527-153306
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                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                       TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial
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Best Local S:
Matches 14
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Indels

Score 13.2; DB 12; Pred. No. 1.8e+03; 0; Mismatches 3;

73.3%;

Length 25;

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TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 245961
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                       1 CGCCATGTCTATTTTGTA 18
                                                                                                                                                                                                                                                                                                           Query Match 73.3'
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-245961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: March
Job time : 447.711 secs
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                                                                      ## Sequence 153326, Application US/11136527
## Publication No. US2005028750A1
## Publication No. US2005028750A1
## GENERAL INFORMATION:
## APPLICANT: Wyeth
## APPLICANT: Wounts, William M
## TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
## TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
## TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
## CURRENT APPLICATION NUMBER: US 11/136,527
## CURRENT APPLICATION NUMBER: US 60/574,294
## PRIOR FILING DATE: 2005-05-26
## NUMBER OF SEQ ID NOS: 362830
## SEQ ID NO 153326
## LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NESCH-136-527-153341

Sequence 153341, Application US/11136527

PUBLICATION NO. US2050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William M

TITLE OF INVENTION:

CURRENT PILING DATE: 2005-05-25

CURRENT PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTHARE: PATENTIN VERSION 3.2

SEQ ID NO 153341

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.4%; Score 13.4; DB 12; Length 25; 93.3%; Pred. No. 1.46+03; tive 0; Mismatches 1; Indels (
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Pred. No. 1.4e+03;
0; Mismatches 1;
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Best Local Similarity 93.3
Matches 14; Conservative
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Matches 14, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Probe US-11-136-527-153326
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial
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                                                                                                                  Sequence 1437211, Application US/11101244

| Bublication No. US2050246794A1
| Publication No. US2050246794A1
| GENERAL INFORMATION:
| APPLICANT: Dharmacon, Inc.
| APPLICANT: Khvorova, Anastasia
| APPLICANT: Reynolds, Angela
| APPLICANT: Reynolds, Angela
| APPLICANT: Marbhall, William
| APPLICANT: Marbhall, William
| APPLICANT: Scaringe, Stephen
| TITLE OF INVENTION: Functional and Hyperfunctional siRNA
| TITLE OF INVENTION: Functional and Hyperfunctional
| FILE REFERENCE: 13499US
| CURRENT FILING DATE: 2005-04-07
| PRIOR APPLICATION NUMBER: 60/502,050
| PRIOR PELING DATE: 2003-09-10
| PRIOR PELING DATE: 2003-09-10
| PRIOR PELING DATE: 2003-09-10
| PRIOR FILING DATE: 2003-10-14
| NUMBER OF SEQ ID NOS: 1591911
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 13; Conserv
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LENGTH: 19
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4, 2006, 03:54:51

Sequence 245961, Application US/11121849
 Publication No. US20050272080A1
 GENERAL INFORMATION:
 APPLICATI: John Palma
 TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded

RESULT 14 US-11-121-849-245961

Adi80196 Human tra

Adf59836 Human pro Ada74096 Equine la Aci55966 Human mic Ack13010 Human mic Ack13010 Human mic Ack13010 Human mic Aca13010 Transcrip Ada20509 Transcrip Adc50505 Human ABC Adm3186 Oligo SEQ Adm3186 Trichinel Adg26421 Brevibact Adr88316 Brevibact Adz6421 Brevibact Adz6421 Brevibact

		c 20	14	77.8	20	12 ADI80196	
	GenCore version 5.1.7	21	13.8	76.7	20		
	Copyright (c) 1993 - 2006 Biocceleration Ltd.	22	13.4	74.4	20	9 ADA74096	
		23	13.4	74.4	25	9 ACI55966	
		c 24	. 13.4	74.4	30	14 AEB14421	
OM nucleic - nucl	OM nucleic - nucleic search, using sw model	25	13.2	73.3	25	9 ACK13008	
		26	13.2	73.3	. 25	9 ACK13010	
Run on:	March 4, 2006, 01:38:40 ; Search time 350.053 Seconds	27	13.2	73.3	25	.9 ACI91047	
	(without alignments)	28	13	72.2	17	2 AAA23223	
	342.704 Million cell updates/sec	29	12.8	71.1	20	12 ADP20509	
		0 30	12.8	71.1	22	3 AAC69355	
	US-09-701-583A-9	31	12.4	68.8	20	12 ADM33186	
Perfect score: 1	118	32	12.4	68.9	32	14 ADY71468	
Seguence:	1 cggcatgtctattttgta 18	33	12.4	68.8	37	12 ADQ26421	
		34	12.4	68.9	37	13 ADR88316	
Scoring table: 1	IDENTITY NUC	c 32	12.2	67.8	18	3 AAZ76976	
•	Gapop 10.0 , Gapext 1.0	36	12.2	67.8	. 18	12 ADQ81512	
		37	12.2	67.8	18	12 ADQ81489	
Searched: 4	4996997 segs, 3332346308 residues	38		67.8	18	12 ADQ81564	
		39	12.2	67.8	20	2 AAQ95371	
Total number of 1	Total number of hits satisfying chosen parameters: 4598950	40	12.2	67.8	20	3 AAK99134	
		c 41	12.2	67.8	20	12 ADJ85601	
Minimum DB seq length: 0	ength: 0	c 42	12.2	67.8	23	9 ACF05388.	
Maximum_DB_seq.1ength:3409	ength/ea/0	c 43	12.2	67.8	23	10 ADC83807	
		C 44	12.2	67.8	23	10 ADF43680	•
Post-processing:	Post-processing: Minimum Match 0%	45	12.2	67.8	24	2 AAQ48628	
	Maximum Match 100%						
•	Listing first 45 summaries					,	
						ALIGNMENTS	ENTS
Database :	N_Geneseq_21:* 1: geneseqn1980s:*						

Add81512 Synthetic Add81549 Synthetic Add8154 DNA oligo Add95371 Primer A Aak99134 20-mer He Adj85601 Nucleic a Acf05388 Rat tumou Acf05388 Rat tumou Add48628 TNF-alpha

			AAQ78423 standard; DNA; 18 BP.				(revised)	(first entry)		TGF-beta gene phosphorothioate antisense oligonucleotide.		Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;	angiogenesis; breast tumour; neurofibroma; glioma;	carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;	Imminiosuppression; origonacieotide; ss.				•		94WO-EP001362.	93EP-00107089.	93EP-00107849.		(BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.		n G, Brysch W, Schlingensiepen K, Schlingensiepen R;		66/44.		10	crearing immunosuppression, rumours, erc.	Claim 6; Page 44; 74pp; English.		The antisense oligonucleotides are useful in the treatment of tumours in	which expression of TGF-beta is of relevance for pathogenicity and/or	
	RESULT 1	AAQ78423		×	AC AAQ78423;	××	_	DT 27-7UN-1995	X	DE TGF-beta gene	XX	KW Transforming g	KW anglogenesis;	•	v. Tumunosoppiess	os synthetic.	XX DN WO9425588-22		PD 10-NOV-1994.		PF 29-APR-1994;	PR 30-APR-1993;	PR 13-MAY-1993;					XX	DR WPI; 1994-358266/44		PT New transforming		PS Claim 6; Page		CC The antisense	-	CC THILDICION OF
																						0						,			,						-
		-											-		oy chance to have a	distribution.				Description	3007004 TOUR			9		_		Aavesseo rer-becaz Aaz65448 Immunosup		4	Adi80039 Human tra	n c	a ro			Aaa23222 Integrin	ACTOUDS HUMBII CLA
TAROR: *	.1990s:*	12000s:*	geneseqn2001as:*	geneseqn2001bs:*	geneseqn2002as:*	geneseqn2002bs:*	geneseqn2003as:*	geneseqn2003bs:*	genesegn2003cs:*	geneseqn2003ds:*	geneseqn2004as:*	geneseqn2004bs:*	geneseqn20058:*	7 H - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	sted. No. 15 the number of februres predicted by chance to mave	score greater than or equal to the score of the result being and is derived by analysis of the total score distribution	STIMMADELES			η DB IĎ	2 2 22078423	, m	8 4 AAD18718	8 14 AEB01186	e	7 5 AAF82681	m (2 AAV4894U 3 AAZ65448	3	12	12 ADI80039	† C	12	6	7	7 2 AAA23222	12 AD180053
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Result

tumours,

gall bladder or duct, pancreas, anus,

colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus breast, ovary, cervix, endometrium, prostate or bladder), liver tumoun malignant melanoma, brain tumours and sarcomas. The oligonuclectides, most of which are directed against TGFbeta or VEGF, are inhibitors of monocyte chemotactic protein-1 (MCP-1) and are useful as anti-inflammatories for treating e.g. asthma, Crohn's disease, ulcerative colitis, diabetes, glomerulomephritis, acute respiratory distress

syndrome and the formation of atherosclerotic plague

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the proliferation of cytotoxic lymphocytes, treatment of endogenous hyperexpression of Gyfotoxic lymphocytes, treatment of endogenous hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas and malignant glioblastomas, treatment and prophylaxis of skin carcinogenesis, and treatment of oesophageal and gastric carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate analogues. (Updated on 25-MAR-2003 to correct PN field.)
of TGF-beta, augmentation of
   the immunosuppressive effect
   888888888888888
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Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

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 100.0%; Score 18; DB 2; Length 18; 100.0%; Pred. No. 26; 0; Indels ive 0; Mismatches 0; Indels
                                                                      1 CGGCATGTCTATTTTGTA 18
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Query Match
Best Local Similarity 100.
Matches 18; Conservative
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Gaps

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AAZ65449 standard; DNA; 18 BP.
        (first entry)
        30-MAR-2000
RESULT 2
 AAZ65449
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Immunosuppressant inhibitor oligonucleotide TGF-beta2-9.

Immunosuppressant inhibitor; transforming growth factor beta; TGF beta; vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer; prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative collitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; ss; atherosclerosis.

Unidentified

W09963975-A2

16-DEC-1999

99WO-EP004013; 10-JUN-1999;

98EP-00110709 98EP-00113974 10-JUN-1998; 25-JUL-1998; (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

Brysch W Schlingensiepen R, Schlingensiepen K,

WPI; 2000-097470/08

Composition containing immune stimulant and inhibitor of agent that adversely affects the immune response, for treating cancers and infections.

Claim 5; Fig 1; 30pp; English.

used in the invention. The invention relates to a composition which contains at least one inhibitor (less than 100 kD) of a substance (e.g. transforming growth factor TGF-beta, vascular endothelial growth factor TGF-beta, vascular endothelial growth factor WBGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors) that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. This oligonucleotide is an example of an inhibitor that is used in the composition. The composition is used as an immunostimulant for the treatment of neoplasms and infections, particularly hyperproliferation; leukaemia, (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi, This sequence is an immunosuppressant inhibitor oligonucleotide, which is

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The invention relates to a mixture comprising an inhibitor or suppressor

of a gene and a molecule binding to an expression product of that gene.

The gene is selected from the group consisting of TGF-beta, erbB-2, MIA,

c-jun, junB, c-fos, VGAM, NF-kappaB p65, NF-kappaB p50, ICAM, VEGF and NF

C-jun, junB, c-fos, VGAM, NF-kappaB p65, NF-kappaB p50, ICAM, VEGF and NF

C-jun, junB, c-fos, Dosphorylated or otherwise modified gene products, have

glycosylated, phosphorylated or otherwise modified gene products, have

cither stimulated or inhibited gene products and/or their derivatives.

The mixture is useful in the preparation of a medicament for treating

tunours, immune disorders or for improving organ or cell transplantation or cell expansion and enhancement or

corgan or cell transplantation or cell expansion and enhancement or

inhibition of immune response is enhanced in a supra-additive manner. The

mixture is useful in drug target validation, i.e., to identify genes that

are relevant for certain pathological state by testing the effect of the

mixture on a cell system or organism. The present sequence is a human
                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mixture useful in preparation of medicament for treating tumors and immune disorders, comprises an inhibitor or suppressor of expression of gene, and a molecule binding to expression product of the gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; TGF-beta; erbB-2; MIA; c-jun; junB; c-fos; VCAM; NF-kappaB p65;
NF-kappaB p50; ICAM; VEGF; NF-kB 2; therapy; tumour; immune disorder;
organ transplantation; cell expansion; drug target validation;
antitumour; immunosuppressive; ss.
                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human oligonucleotide #4, useful in drug target validation.
                                                                                                                                                                                                        DB 3; Length 18;
                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                    Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                        100.0%; Score 18; DB 100.0%; Pred. No. 26;
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                                                                                                                                                                                                                                                                                                                                                                                                              AAD18718 standard; DNA; 18
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                                                                                                                                                                                                                                             18; Conservative
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                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
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Gaps

明治を行う

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The invention relates to a pharmaceutical composition (PC) comprising one or more stimulators that stimulate the function of immune system and/or immune cells and or more substances inhibiting cell proliferation and/or inducing cell death. A pharmaceutical composition is useful for treating neoplaems chosen from solid tumors; blood born tumors such as leukemias, acute or chronic myelotic or lymphoblastic leukemia; tumor metastessis; benign tumors; or 1s chosen from bile duct carcinoma, brach tumors; or 1s chosen from bile duct carcinoma, carcinoma, brain tumors; or 1s chosen from bile duct carcinoma, bladder carcinoma, embryonal carcinoma, epithelial carcinoma, esophageal carcinoma, embryonal carcinoma, colon carcinoma, esophageal carcinoma, entropial carcinoma, gallbladder carcinoma, agentic carcinoma, head and neck carcinoma, carcinoma, ung carcinoma, medilary carcinoma, non-small cell bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pharmaceutical composition useful for treating neoplasm, comprises stimulators stimulating function of immune system and/or immune cells and substances inhibiting cell proliferation and/or inducing cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, eintestine carcinoma, rectal carcinoma, renal cell carcinoma, skin carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine carcinoma, rheumatoid arthritis and psoriasis. The present sequence represents a TGF-beta 2 inhibition oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical; cell death, neoplasm; ss; Cytostatic; Apoptotic; Immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic;
                                                                                                                                  ö
                                                                                       4; Length 18;
                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGF-beta 2 inhibition oligonucleotide SEQ ID NO 30.
                                             Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;
oligonucleotide useful in drug target validation
                                                                                   Query Match 100.0%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 26; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlingensiepen K, Schlingensiepen R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 30; 46pp; English
                                                                                                                                                                        1 CGCCATGTCTATTTTGTA 18
                                                                                                                                                                                                                   CGCCATGTCTATTTGTA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGF-beta antagonist; Vaccine.
                                                                                                                                                                                                                                                                                                                           AEB01186 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ANTI-) ANTISENSE PHARMA GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-2003; 2003EP-00029367.
05-FEB-2004; 2004US-0541771P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-2004; 2004WO-EP053604
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-479334/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2005059133-A2.
                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                     AEB01186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used in the invention. The invention relates to a composition which contains at least one inhibitor (less than 100 kD) of a substance (e.g. transforming growth factor TGF-beta, vascular endothelial growth factor VEGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors) that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. The oligonucleotide is an example of an inhibitor that is used in the
                                                                                                                                                                                                                                                                                                                                                               Immunosuppressant inhibitor, transforming growth factor beta, TGF beta, vascular endochelial growth factor; VBGF, interleukin-10; IL-10; cancer; prostaglandin E2; PGE2; immune response, tumour; asthma, Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative colitis, diabetes; glomerulonephritis; acute respiratory distress syndrome; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       composition. The composition is used as an immunostimulant for the treatment of neoplamms and infections, particularly Myperproliferation, leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi, colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours malignant melanoma, brain tumours and sarcomas. The oligonucleotides, most of which are directed against TGFbeta or VBGF, are inhibitors of
                                         Gaps
                                                                                                                                                                                                                                                                                                                             Immunosuppressant inhibitor oligonucleotide TGF-beta-12-9/22-2263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatories for treating e.g. asthma, Crohn's disease, ulcerat. colitis, diabetes, glomerulonephritis, acute respiratory distress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition containing immune stimulant and inhibitor of agent adversely affects the immune response, for treating cancers and
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
 Score 18; DB 14; Length 18;
Pred. No. 26;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 18; DB 3; Length 22; 100.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       syndrome and the formation of atherosclerotic plague
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22 BP; 4 A; 3 C; 7 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brysch W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schlingensiepen R,
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Fig 1; 30pp; English.
                                                                               78
                                                                                                   CGGCATGTCTATTTTGTA 18
100.0%;
ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98EP-00110709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-EP004013
                                                                                                                                                                                                               AAZ65511 standard; DNA; 22
                                                                               1 CGGCATGTCTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-097470/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schlingensiepen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
 Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-1998;
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                                                                                                                                                                                                                                                                                           30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infections.
                                                                                                                                                                                                                                                     AAZ65511;
                                                                                                                                                                       RESULT 5
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Sequence 18 BP; 3 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

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Immunosuppressant inhibitor; transforming growth factor beta; TGF beta; vascular endochelial growth factor; VBGF; interleukin-10; IL-10; cancer; yorstaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative collitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition containing immune stimulant and inhibitor of agent that adversely affects the immune response, for treating cancers and
                                                                                                        Immunosuppressant inhibitor oligonculeotide TGF-beta2-9/1.
                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Fig 1; 30pp; English.
              AAZ65472 standard; DNA; 16 BP
                                                                          30-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-097470/08
                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlingensiepen K,
                                                                                                                                                                                                                     atherosclerosis.
                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                              WO9963975-A2
                                                                                                                                                                                                                                                                                                                                         10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                       10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                       25-JUL-1998;
                                                                                                                                                                                                                                                                                                            16-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infections.
                                              AAZ65472;
   AAZ65472
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence was used in reverse transcriptase polymerase chain reaction (RT-PCR) analysis of human prostate cancer cells. The invention relates to an isolated polymuclectide comprising a prostate-specific chimeric enhancer (PSB) sequence and a proximal promoter sequence operably linked to a nucleic acid segment that encodes a heterologous polymepicide. The PSB contains an ARE and specifically activates transcription of the nucleic acid segment in a mammalian prostate cell. The construct is useful for the treatment of a prostate disorder or a metastasised prosefate cancer, such as hyperplasia or hyperproificration of prostate cells. It is also useful for directing the tissue-specific expression of a heterologous polypeptide in a human prostate cell. The construct may be administered by injection, infection, transformation, niposome-mediated transfection, polybrene-mediated transfection, receptor mediated uptake or Ca-PO4-mediated transfection, receptor
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide, useful for treating prostatic cancer, comprises prostate specific chimeric enhancer and proximal promoter sequence operably linked to nucleic acid encoding heterologous polypeptide.
                                                                                                                                                                                                                                                            Human; androgen response element; ARE; cytostatic; gene therapy; prostate-specific chimeric enhancer; transcriptional regulation; targeted gene expression; prostate cancer; prostate disorder. prostate-specific antigen; PSA; transforming growth factor beta2;
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 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27 BP; 5 A; 7 C; 6 G; 9 T; 0 U; 0 Other;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 73; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu L, Carey MF, Belldegrun AS;
   ö
                            1 CGGCATGTCTATTTTGTA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA SYSTEM
                                                          ceccarercrarrigra 22
                                                                                                                                       BP
                                                                                                                                                                                                                              Human TGF-beta2 PCR primer #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                13-OCT-2000; 2000WO-US028444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0159691P.
99US-0159730P.
                                                                                                                                       AAF82681 standard; DNA; 27
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                         IGF-beta2; PCR primer; ss
 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-273768/28.
                                                                                                                                                                                                                                                                                                                                                                                     WO200127256-A2.
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-OCT-1999;
15-OCT-1999;
                                                                                                                                                                                                   18-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Matches
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Brysch W;

Schlingensiepen R,

99WO-EP004013

98EP-00113974

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This sequence is an immunosuppressant inhibitor oligonucleotide, which is used in the invention. The invention relates to a composition which contains at least one inhibitor (less than 100 kD) of a substance (e.g. transforming growth factor TGF-beta, vascular endothelial growth factor VBGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors) that adversely affects the immune response. The composition The composition is used as an immunostimulant for the creatment of neoplasms and infections, particularly hyperproliferation; leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi, colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder); liver tumours, malignant melanoma, brain tumours and sarcomae. The oligonucleotides, most of which are directed against TGFbeta or VBGF, are inhibitors of monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
inflammatories for treating e.g. astehma, Crohn's disease, ulcerative colitis, diabetes, glomerulonephritis, acute respiratory distress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.9%; Score 16; DB 3; Length 16; 100.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       syndrome and the formation of atherosclerotic plaque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16 BP; 2 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGCATGTCTATTTG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV48940 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCATGTCTATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 16; Conserv
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ID AAV4
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Gaps

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CGGCATGTCTATTTTGTA 18

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Best Local Similarity 100. Matches 18; Conservative

20

CGGCATGTCTATTTTGTA

* RESULT 7

的人名意格 人名塞克斯森

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Preparation of antisense oligo:nucleotide(s) which lack long runs of consecutive guanosine or inosine - and have. specific ratio of residues able to form two or three hydrogen bonds, heve greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in
                                                                 Transforming growth factor-beta2; TGF-beta2; antisense oligonucleotide; modulate; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
                                              IGF-beta2 antisense oligonucleotide TGF-beta2-11.
                                                                                                                                                                                                     (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                                                                                                                                                                                        Claim 10; Fig 8a; 286pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stimulating the immune system
                                                                                                                                                                                                                          Brysch W;
                                                                                                                                                                97EP-00101531
                                                                                                                                                                                   97EP-00101531
                           15-OCT-1998 (first entry)
                                                                                                                                                                                                                                            WPI; 1998-400910/35.
                                                                                                                                                                                                                         Schlingensiepen K,
                                                                                                         Homo sapiens
                                                                                                                                                                31-JAN-1997;
                                                                                                                                                                                   11-JAN-1997;
                                                                                                                           EP856579-A1.
                                                                                                                                             05-AUG-1998
                                                                                              Synthetic.
         AAV48940;
                                                                                                                                                                                                                                                                                                     culture
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transforming growth factor-beta2 (TGF-beta2). Of these, only cligonucleotides ANV48930-67 resulted in significant redcution in TGF-beta 2 protein expression, while oligonucleotides ANV48968-49007 had little effect. The oligonucleotides exemplify the invention in TGF-beta 2 protein expression, while oligonucleotides that contain 8-30 nucleotides, which contain at most B nucleotides that can each form three Hydrogen bonds to cytosine; B nucleotides that can each form three Hydrogen bonds to cytosine; do not contain four consecutive mucleotides able to form three H-bonds each to four consecutive cytosines; do not contain two sequences of three consecutive nucleotides each able to form three H-bonds each (2R) or three such bonds (3R) is given by 2R,3R to form two. H-bonds each (2R) or three such bonds (3R) is given by 2R,3R consecutive cytosines, and the ratio between residues able to form two. H-bonds each (2R) or three such bonds (3R) is given by 2R,3R consecutive particularly the genes for p53. ErB-2, junB, junD, TGF-beta 1 or beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The oligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and control proliferation contains to the appear of cancer or (targeting TGF) for the advance of proteins (by altering their expression or activity) and contains the c
AAV48930-49007 represent antisense oligonucleotides directed against
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Score 16; DB 2; Length 20;
Pred. No. 2.7e+02;
0; Mismatches 0; Indels
 88.5%,
100.0%; Pre-
0;
                        Conservative
         Local Similarity
les 16; Conserv
Query Match
                       Matches
                                                8
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GCATGTCTATTTTGTA 18

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AAZ65448 RESULT 9
AAZ65448
ID AAZ6
XX
AC AAZ6

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AAZ65448 standard; DNA; 20 BP.
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30-MAR-2000 (first entry)

Immunosuppressant inhibitor, transforming growth factor beta; TGF beta; vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer; prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative collitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; ss; Immunosuppressant inhibitor oligonucleotide TGF-beta2-8.

atherosclerosis.

Unidentified

W09963975-A2

99WO-EP004013 10-JUN-1999;

98EP-00110709 98EP-00113974 10-JUN-1998; 25-JUL-1998;

Schlingensiepen K, Schlingensiepen R, Brysch W;

(BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

WPI; 2000-097470/08

Composition containing immune stimulant and inhibitor of agent that adversely affects the immune response, for treating cancers and infections.

Claim 5; Fig 1; 30pp; English.

This sequence is an immunosuppressant inhibitor oligonucleotide, which is used in the invention. The invention relates to a composition which contains at least one inhibitor (less than 100 kD) of a substance (e.g. transforming growth factor TGF-beta, vascular endothelial growth factor TGF-beta, vascular endothelial growth factor (bright interleukin-10 IL-10, prostaglandin B2 PGE2, or their receptors) that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. This oligonucleotide is an example of an inhibitor that is used in the treatment of neoplasms and infections, particularly hyperproliferation; leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi, colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours, consistent and sarcomas The oligonucleotides. of which are directed against TGFbeta or VEGF, are inhibitors of Crohn's disease, ulcerative inflammatories for treating e.g. asthma, Crohn's disease, ulcerat colitis, diabetes, glomerulonephritis, acute respiratory distress syndrome and the formation of atherosclerotic plaque nonocyte chemotactic protein-1

Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

. 0 88.9%; Score 16; DB 3; Length 20; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels Query Match 88.9%; Best Local Similarity 100.0%; Matches 16; Conservative 0

Gaps

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RESULT 10 AAZ65509

AAZ65509 standard; DNA; 20

AAZ65509;

30-MAR-2000 (first entry)

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This sequence is an immunosuppressant inhibitor oligonucleotide, which is used in the invention. The invention relates to a composition which contains at least one inhibitor (less than 100 kD) of a substance (e.g. transforming growth factor TGF-beta, vascular endothelial growth factor VBGF, interleukin-10 IL-10, prostaglandin E2 PGE2, or their receptors) that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. This composition is an example of an inhibitor that is used in the treatment of neoplasms and infections, particularly hyperproliferation; leukaemia, (non-)Hodgkin's lymphoma, carcinoma (of oesophagus, bronchi,
                                      Immunosuppressant inhibitor; transforming growth factor beta; TGF beta; vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer; prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative collitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            colon-rectum, stomach, intestine, gail bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours, malignant melanoma, brain tumours and sarcomas. The oligonucleotides, most of which are directed against TGRbeta or VEGF, are inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatories for treating e.g. asthma, Crohn's disease, ulcerative colitis, diabetes, glomerulonephritis, acute respiratory distress syndrome and the formation of atherosclerotic plaque
Immunosuppressant inhibitor oligonucleotide TGF-beta-12-9/20-2261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition containing immune stimulant and inhibitor of agent adversely affects the immune response, for treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MCP-1) and are useful as anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 3 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schlingensiepen R, Brysch W;
                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Fig 1; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monocyte chemotactic protein-1
                                                                                                                                                                                                                                                                                                                                  99WO-EP004013.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schlingensiepen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-097470/08
                                                                                                                                                        atherosclerosis
                                                                                                                                                                                                                                            W09963975-A2
                                                                                                                                                                                                                                                                                                                                  10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-1998;
                                                                                                                                                                                                                                                                                       16-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections.
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antisense; transforming growth factor; TGF; beta 2; TGF-beta 2; cytostatic; nootropic; neuroprotective; immunosuppressive; hyperproliferative disorder; cancer; neurodegenerative; hyperactivation; Gaps Human transforming growth factor-beta 2 antisense oligo, SEQ ID No ö 88.9%; Score 16; DB 12; Length 20; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other; ilarity 100.0%; P. Conservative 0; BP 16 ADI80039 standard; DNA; 20 (first entry) 1 CGGCATGTCTATTTG Local Similarity 22-APR-2004 ADI80039; Query Match RESULT 12 ADI80039 셤 8 ö

Gaps

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0; Indels

100.0%; Pred. ...

16; Conservative

88.98;

Query Match Local CGGCATGTCTATTTG 16 cecentriciarinie 20

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Score 16; DB 3; Length 20; Pred. No. 2.7e+02;

Human transforming growth factor-beta 2 target DNA region, SEQ ID No 185.

(first entry)

22-APR-2004

ADI80184;

AD180184/c
ID AD18(
XX
AC AD18(
XX
XX
XX
DT 22-A8
XX
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XX
XX

ВР

ADI80184 standard; DNA; 20

RESULT 11

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The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-bera 2, and inhibits the expression of TGF-bera 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, nootropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition
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antisense; transforming growth factor; TGF; beta 2; TGF-beta 2; cytostatic; nootropic; neuroprotective; immunosuppressive; hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compounds, particularly antisense oligonucleotides targeted to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 16; SEQ ID NO 185; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              Dobie KW;
                                                                                                                                                                                                                                                         02-JUL-2002; 2002US-00189267.
                                                                                                                                                                                                                                                                                                 02-JUL-2002; 2002US-00189267
                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                              Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-081742/08
                                                                    immune; ss; human
                                                                                                                                                              US2004006030-A1
                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              Monia BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune
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Schlingensiepen R;

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The invention relates to a pharmaceutical composition (PC) comprising one or more stimulators that stimulate the function of immune system and/or immune cells and one or more substances inhibiting cell proliferation and/or inducing cell death. A pharmaceutical composition is useful for treating neoplasms chosen from solid tumors, blood born tumors such as leukemias, acute or chronic myelotic or lymphoblastic leukemia; tumor metastasis; benign tumors; or is chosen from bile duct carcinoma, brain tumors, or is chosen from bile duct carcinoma, badder carcinoma, embryonal carcinoma, epithelial carcinoma, esophageal carcinoma, embryonal carcinoma, color carcinoma, colorectal carcinoma, endometrial carcinoma, gastric carcinoma, head and neck carcinoma, liver carcinoma, pung carcinoma, medullary carcinoma, pancess carcinoma, liver carcinoma, pancess carcinoma, liver carcinoma, papillary carcinoma, prostate carcinoma, papillary adenocarcinoma, prostate carcinoma, small cell carcinoma, papillary carcinoma, rectal carcinoma, renal cell carcinoma, small call carcinoma, small call carcinoma, small cell carcinoma, small call carcinoma, small call carcinoma, small cell carcinoma, small cell carcinoma, small call carcinoma, small cell carcinoma, car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pharmaceutical composition useful for treating neoplasm, comprises stimulators stimulating function of immune system and/or immune cells and substances inhibiting cell proliferation and/or inducing cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine carcinoma, rheumatoid arthritis and psoriasis. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents a TGF-beta 2 inhibition oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 29; 46pp; English
                                                                                                                                                                                                                                                                                                                                                         (ANTI-) ANTISENSE PHARMA GMBH
                                                                                                                                                                                                                                    19-DEC-2003; 2003EP-00029367.
                                                                                                                                                         20-DEC-2004; 2004WO-EP053604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2005-479334/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Schlingensiepen K,
    WO2005059133-A2
                                                                                   30-JUN-2005
    The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-berg 2, and inhibits the expression of TGF-berg 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-80 nucleobase portion of an active site on a nucleic acid molecule encoding TGF-berg 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-betg 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-berg 2 is inhibited; treating an animal having a disease or condition associated with TGF-berg 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-berg 2 is inhibited; amount of the compound so that expression of TGF-berg 2 is inhibited; amount of the compound so that expression of TGF-berg 2 is inhibited; amount of the compound so that expression of TGF-berg 2 is inhibited; amount of the compound so that expression of TGF-berg 2 is inhibited; amount of the compound. The antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polynucleotide sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.9%; Score 16; DB 12; Length 20; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 15; SEQ ID NO 40; 135pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dobie KW;
                                                                                                                                                                                                                                                                                                                   02-JUL-2002; 2002US-00189267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Freier SM,
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immune; ss; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune response.
                                                                                                                                                     US2004006030-A1
                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                               Mouse transforming growth factor-beta 2 target DNA region, SEQ ID No 243.
                                                                                                                                                                                                                                                                     antisense; transforming growth factor; TGF; beta 2; TGF-beta 2; cytostatic; nootropic; neuroprotective; immunosuppressive; hyperproliferative disorder; cancer; neurodegenerative; hyperactivation; immune; ss; mouse; murine.
                                Gaps
                               ;
Query Match 88.9%; Score 16; DB 14; Length 20; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                             ВР
                                                                          1 GCATGTCTATTTTGTA 16
                                                                                                                                             ADI80242/c
ID ADI80242 standard; DNA; 20
                                                                                                                                                                                                                    (first entry)
                                                           3 GCATGTCTATTTTGTA
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                                                                                                                                                                                         ADI80242;
                                                                                                                                 RESULT 14
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Gaps

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1 CGGCATGTCTATTTG 16 CGGCATGTCTATTTG 20

16; Conservative

Best Local Similarity

Matches

JS2004006030-A1 Mus musculus.

pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic; Immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic; TGF-beta antagonist; Vaccine.

Synthetic

TGF-beta 2 inhibition oligonucleotide SEQ ID NO 29.

X S X & & & S E X D X S X D

08-SEP-2005 (first entry)

AEB01185;

AEB01185 standard; DNA; 20 BP

RESULT 13 AEB01185

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08-JAN-2004

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compound. The antisense compound has cytostatic, noctropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition associated with TGF-bera 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents a preferred target DNA region of TGF-beta 2 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel antisense compound of 8-80 nucleobases and in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to:

a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and acarrier or diluent; inhibiting the expression of TGF-beta 2 in calls or tissues by contacting the cells or tissues with the compound so that disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 16; SEQ ID NO 243; 135pp; English.
                                                                                                                                                                                                                                                                                                            Dobie KW
02-JUL-2002; 2002US-00189267.
                                                                                                     02-JUL-2002; 2002US-00189267.
                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                            Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-081742/08
                                                                                                                                                                                                                                                                                                            Monia BP,
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                               Gaps
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82.2%; Score 14.8; DB 12; Length 20; 88.9%; Pred. No. 1.1e+03; ive 0; Mismatches 2; Indels (
                                                              1 CGGCATGTCTATTTTGTA 18
                               16; Conservative
Query Match
Best Local Similarity
                               Matches
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20 CGGCATGTCGATTTTATA 3 ઠ

ADI80115 standard; DNA; 20 BP ADI80115; RESULT 15 ADI80115

(first entry) 22-APR-2004

antisense; transforming growth factor; TGF; beta 2; TGF-beta 2; cytostatic; nootropic; neuroprotective; immunosuppressive; hyperproliferative disorder; cancer; neurodegenerative; hyperactivation; Mouse transforming growth factor-beta 2 antisense oligo, SEQ ID No 116. immune; ss; mouse; murine

Mus musculus

US2004006030-A1.

08-JAN-2004.

02-JUL-2002; 2002US-00189267.

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The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-bera 2, and inhibits the expression of TGF-bera 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-bera 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-bera 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-bera 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense compound. The antisense compound has cytostatic, nootropic, compound, composition and methods are useful for treating a disease or condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated with TGF-beta 2, such as a hyperproliferative disorder e.g. cancer, a neurodegenerative disorder, or a disease or condition involving hyperactivation of an immune response. This polynucleotide sequence represents an antisense oligonucleotide of the invention.
                                                                                                                                                                                                                                              nucleic acid encoding TGF-beta 2, useful for treating cancer, a
neurodegenerative disorder, or a disease involving hyperactivation of
                                                                                                                                                                                                                    compounds, particularly antisense oligonucleotides targeted to a
                                                                                                                                                                                                                                                                                                                                                       Example 16; SEQ ID NO 116; 135pp; English
                                                                                                           Dobie KW;
02-JUL-2002; 2002US-00189267
                                                     (ISIS-) ISIS PHARM INC
                                                                                                           Monia BP, Freier SM,
                                                                                                                                                            WPI; 2004-081742/08
                                                                                                                                                                                                                                                                                                          immune response.
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82.2%; Score 14.8; DB 12; Length 20; 88.9%; Pred. No. 1.1e+03; Mismatches ..0 1 CGCCATGTCTATTTTGTA 18 Local Similarity 88.9 Query Match Matches ò

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Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

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Gaps ô

Indels

4, 2006, 02:31:45 Search completed: March Job time : 353.053 secs

OM nucleic

Run on:

Sequence:

Minimum DB Maximum DB

Database

Searched:

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PAT 22-JAN-2000
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              AR232822 Sequence
AX008980 Sequence
AX030117 Sequence
AX316438 Sequence
A89126 Sequence
BBD066639 An antise
BD234925 A method
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CC846845
AX222950
CQ924659
CC924659
CS107636
CS107636
AX78553
AX78553
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AX78553
CG865510
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Pred: No. 41;
; Mismatches 0; Indels
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Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLEOTIDE PREPARATION METHOD
PATCH: WO 9833904-A 532 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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Sequence 532 from Patent BP0856579.
A90351
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Sequence 532 from Patent WO9833904.
A88384

    .20
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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                                         AX316438
A89126
BD0666
BD034925
AX008996
CQ846845
AX22760
AX802950
CQ924659
CS116412
AX224286
CS116412
AX785539
AX785539
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AX785543
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100.0%; Pr
:ive 0;
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unclassified sequences.
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Best Local Similarity 100.
Matches 20; Conservative
unidentified
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                                                                                    DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                      DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                             RESULT 1
A88384
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                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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A90351
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A90351 Sequence 53
BD05897 An antise
BD24910 A method
CS123684 Sequence
AX008981 Sequence
AX252495 Sequence
A89125 Sequence
A89125 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX008995 Sequence
A89127 Sequence 12
BD066640 Am antise
BD234926 Amethod
AX008997 Sequence
A40542 Sequence 79
A89067 Sequence 12
BD066580 Am antise
                                                        4, 2006, 01:42:16; Search time 957.368 Seconds (without alignments) 1187.494 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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        5.1.7
Biocceleration Ltd.
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       GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                        nucleic search, using sw model
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Gaps

o No Result

us-09-701-583a-14.sz40.rge

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PAT 16-JUL-2005
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00,AGIP35/00,
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antisense oligonucleotide"
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SN, WOLFGANG PI
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                                                                                                                      OS Homo sapiens (human)
PN JP 2002517434-A/14
PD 18-JUN-2002
PF 10-JUN-1999 JP 2000553044
PR 10-JUN-1999 EP 98110709.7,25-JUL-1998 EP 98113974.4 | KARL HERMANN SCHLINGENSIEPEN, WOLFGANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schlingensiepen, K.H.

Combination therapy associating a tgf-beta antagonist with
Chemotherapeutic agent
Patent: WO 2005059133-A 35 30-JUN-2005;
Antisense Pharma GmbH (DE)
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                            BRYSCH

PC A61K45/06,A61K31/7088,A61K38/00,A61K39/395,A61K39/395

PC 00,A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC

method for stimulating the immune system

FH Key Location/Qualifiers

FT source / organism='Homo sapiens (human)'
                           (1) (Dates 1 to 20)
Schlingensiepen, R. and Brysch, W. Schlingensiepen, R. and Brysch, W. Schlingensiepen, R. timulating the immune system
Patent: JP 202517434-A 14 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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synthetic construct
                  Hominidae; Homo
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS Schlingensiepen, K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 201511000-A 532 07-AUG-2001,
BLOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS UNKNOWN GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
PN 30-JAN-1998 JP 1998532533
PR 31-JAN-1998 JP 1998532533
PR 31-JAN-1997 RP 971015-7
PI KARL HERNANN SCHITTING
PC C12N15/11
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31-0JAN-1998 DP 1998532533
31-JAN-1999 BP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N1s/11,C07H21/04,A6IK31/70
An antisenee oligonucleotide preparation method FH
Location/Qualifiers
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Pred. No. 41;
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Pred. No. 41;
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1 (bases 1 to 20)
Brysch, W.D. and Schlingensiepen, K.D.
An antisense oligonucleotide preparation method
Patent: EP 0856579-A 532 05-AUG-1998;
BIOGNOSTIK GES (DE)
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100.0%; Score 20; DE
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches

    .20
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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/mol_type="genomic DNA"
/db xref="taxon:32644"
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JP 2002517434-A/14.
Homo sapiens (human)
Homo sapiens
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1 Similarity 100.0%;
20; Conservative 0;
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PAT 27-AUG-2002

REFERENCE AUTHORS JOURNAL

FEATURES

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1 (bases 1 to 18)
Schlingensiepen, K.H. and Brysch, W.
An antisense Oligonucleotide preparation method
Patent: JP 2001511000-A 1273 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S1-JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N15/11,C07121/04,A61K31/70
An antisense oligonucleotide preparation method FH
Location/Qualifiers
                                                                                                                                                                                                                                                                     Score 18; DB 6; Length 18;
Pred. No. 4.6e+02;
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                                                             1 (bases 1 to 18)
Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
PATENT: WO 9833904-A 1273 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
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An antisense oligonucleotide preparation method.
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A method for stimulating the immune system.
BD234924 '
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    .18
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    /db_xref="taxon:32644"

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/organism="unidentified"
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/db_xref="taxon:32644"
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07-AUG-2001
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                                                 unclassified sequences.
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JP 2002517434-A/28.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                             Brysch, W., Schlingensiepen, K.H. and Schlingensiepen, R. A method for stimulating the immune system Patent: WO 9963975-A 14 16-DEC-1999, BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mixture comprising an inhibitor or suppressor of a gene and a molecule binding to an expression product of that gene abtent: WO 0168146.A $ 5.0-SEP-2001; Biognostik Gesellschaft fuer biomelekulare Diagnostik mbH (DE)
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Pred. No. 41;
               linear
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Sequence 1273 from Patent WO9833904.
A89125 GI:6737695
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                                                                                                                                                                                                                                                                                                                                      /mol_type="unassigned DNA"
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/db_xref="taxon:9606"
AX008981 20 bp
Sequence 14 from Patent WO9963975.
AX008981
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/organism="Homo sapiens"
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Sequence 5 from Patent WO0168146.
AX252495
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100.0%;
                                                               AX008981.1 GI:9996355
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Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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AUTHORS TITLE

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Schlingensiepen, K.H. and Brysch, W.
An antisense Oligonucleotide preparation method
Patent: JP 2001511000-A 1275 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP 2001511000-A/1275
07-AUG-2001
31-ANA-1998 JP 1998532533
31-JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEBEN, WOLFGANG BRYSCH
C12N15/11, CO7721/04, A61K31/70
An antisense oligomucleotide preparation method FH
Location/Qualifiers
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                                              linear
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                                                                                                                                                      unclassified sequences.

1 (bases 1 to 16)

Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD PATENT: WO 8313904-A 1275 06-AUG-1998;

BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)

Location/Qualifiers
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                                              DNA
                                             16 bp DN
Sequence 1275 from Patent WO9833904.
A89127
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    .16
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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/organism="unidentified"
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/db_xref="taxon:32644"
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A61P35/00,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
A61P3 for stimulating the immune system
Key
                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                         18-JUN-2002
10-JUN-1999 JP 2000553044
10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI
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                                                                                           Schlingensiepen, K. H., Schlingensiepen, R. and Brysch, W. A method for stimulating the immune system Patent: 19 20022144 2 8 18 -JUN -2002. BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
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Location/Qualifiers
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/mol_type="unassigned DNA"
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Matches 18; Conservative 0; Mismatches
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                              Homo sapiens (human)
JP 2002517434-A/28
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Homo sapiens
Homo sapiens (human)
Homo sapiens
                                                               Hominidae; Homo.
1 (bases 1 to 18)
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AX008995
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                                                                                 BD234926.1 GI:33044696
JP 2002517434-A/30.
Homo sapiens (human)
Homo sapiens (buman)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
JP 2002517434-A/30
18-JUN-2002
10-JUN-1999 JP 2000553044
10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG PI
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A method for stimulating the immune system
Patent: WO 9963975-A 30 16-DEC-1999;
BIOGNOSTIK GES (DE): BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
Location/Qualifiers
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PC 00,A61P35/00,
PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC method for stimulating the immune system FH Key Location/Qualifiers FT source 1.16
                                                                                                                                                                                                          (bases 1 to 16)
Schlingenslepen, R. and Brysch, W. A method for stimulating the immune system
Patent: JP 202517434-A 30 18-JUN-2002;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
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Location/Qualifiers
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1 Similarity 100.0%; Pred. No. 5.1e+
16; Conservative 0; Mismatches

    .16
    /organism="Homo sapiens"
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/db_xref="taxon:9606"

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Sequence 30 from Patent WO9963975.
AX008997.1 GI:9996371
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                    COMMENT
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ORIGIN

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specification describes oligonucleotides that contain 8-30 mucleotides, which contain at most 8 nucleotides that contain 8-30 mucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; 40 not contain four consecutive mucleotides able to form three H-bonds each to four consecutive cytosines; 40 not contain two sequences of three consecutive nucleotides each able to form three H-bonds each (2R) or three each able to form three H-bonds each (2R) or three such bonds to three residues able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The oligonucleotides are used to modulate expression of beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The oligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and the immune system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunosuppressant inhibitor; transforming growth factor beta, TGF beta, vascular endothelial growth factor; VBGF; interleukin-10; IL-10; cancer; prostaglandin E2: pGE2; immune response, tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative collitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                             Score 20; DB 2; Length 20; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunosuppressant inhibitor oligonucleotide TGF-beta2-14.
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCTTTCACCAAATTGGAAGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCTTTCACCAAATTGGAAGC 20
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                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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98EP-00113974
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                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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25-JUL-1998;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mixture useful in preparation of medicament for treating tumors and immune disorders, comprises an inhibitor or suppressor of expression of a gene, and a molecule binding to expression product of the gene.
that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. This oligonucleotide is an example of an inhibitor that is used in the composition. The composition is used as an immunostimulant for the treatment of neoplasms and infections, particularly hyperproliferation; colon-rectum, stomach, intestine, gall bladder or duct, pancreas, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours malignant melanoma, brain tumours and sarcomas. The oligonucleotides, malignant melanoma, brain tumours and sarcomas. The oligonucleotides, monocyte chemotactic protein-1 (MCP-1) and are useful as anti-inflammatories for treating e.g. asthma, Crohn's disease, ulcerative colitis, diabetes, glomerulonephritis, acute respiratory distress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; TGF-beta; erbB-2; MIA; c-jun; junB; c-fos; VCAM; NF-kappaB p65; NF-kappaB p50; ICAM; VBGF; NF-kB 2; therapy; tumour; immune disorder; organ transplantation; cell expansion; drug target validation; antitumour; immunosuppressive; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human oligonucleotide #5, useful in drug target validation.
                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; DB 3; Length 20; 100.0%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                        syndrome and the formation of atherosclerotic plaque
                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                        20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pharmaceutical composition useful for treating neoplasm, comprises stimulators stimulating function of immune system and/or immune cells and substances inhibiting cell proliferation and/or inducing cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a pharmaceutical composition (PC) comprising one or more stimulators that stimulate the function of immune system and/or immune cells and one or more substances inhibiting cell proliferation and/or inducing cell death. A pharmaceutical composition is useful for treating neoplasms chosen from solid tumors; blood born tumors such as
or cell expansion, where inhibition of tumour growth, improvement of organ or cell transplantation or cell expansion and enhancement or inhibition of immune response is enhanced in a supra-additive manner. The mixture is useful in drug target validation, i.e., to identify genes that are relevant for certain pathological state by testing the effect of the mixture on a cell system or organism. The present sequence is a human oligonucleotide useful in drug target validation
                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptot
[mmunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic;
                                                                                                                                                                                                                Score 20; DB 4; Length 20;
Pred. No. 4.3;
                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGF-beta 2 inhibition oligonucleotide SEQ ID NO 35.
                                                                                                                                                                        Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       0; Mismatches
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGF-beta antagonist; Vaccine
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEB01191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunosuppressant inhibitor; transforming growth factor beta; TGF beta; vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer; prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; monocyte chemocactic protein-1; MCP-1; ulcerative collitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours malignant melanoma, brain tumours and sarcomas. The oligonucleotides, most of which are directed against TGPbeta or VEGF, are inhibitors of monocyte chemotactic protein-1 (MCP-1) and are useful as anti-
                                                                                                                                                              Gaps
  testicular carcinoma, uterine
soriasis. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatories for treating e.g. asthma, Crohn's disease, ulcerat. colitis, diabetes, glomerulonephritis, acute respiratory distress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition containing immune stimulant and inhibitor of agent tadversely affects the immune response, for treating cancers and
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                                                                                                                     Score 20; DB 14; Length 20;
Pred. No. 4.3;
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                                                                                                                                                              Indels
carcinoma, sebaceous gland carcinoma, testicular ca
carcinoma, rheumatoid arthritis and psoriasis. The
represents a TGF-beta 2 inhibition oligonucleotide.
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                                                                                 Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                              Mismatches
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                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                            AAZ65468 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                              Conservative
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                                                                                                                                   Local Similarity
wes 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
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Matches
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carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell

DB 12; Length 20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel antisense compound of 8-80 nucleobases in length targeted to, and which specifically hybridizes with, a nucleic acid molecule encoding transforming growth factor (TGF)-beta 2, and inhibits the expression of TGF-beta 2. The invention further relates to: a compound 8-80 nucleobases in length that specifically hybridizes with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding TGF-beta 2; a composition comprising the compound and a carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or tissues by contacting the cells or tissues with the compound so that expression of TGF-beta 2 is inhibited; treating an animal having a disease or condition associated with TGF-beta 2 by administering to the animal a therapeutic or prophylactic amount of the compound so that expression of TGF-beta 2 is inhibited; and screening an antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; nootropic; neuroprotective; immunosuppressive; hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compound. The antisense compound has cytostatic, nootropic, neuroprotective, and immunosuppressive activities. The compound, composition and methods are useful for treating a disease or condition
                                                                                                                                                                                                                                                                                                                                                                                                      Human transforming growth factor-beta 2 antisense oligo, SEQ ID No 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid encoding TGF-beta 2, useful for treating cancer, a
neurodegenerative disorder, or a disease involving hyperactivation of
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New compounds, particularly antisense oligonucleotides targeted to a
                                                                                                                                                                                                                                                                                                                                                                                                                                          antisense; transforming growth factor; TGF; beta 2; TGF-beta 2;
                                                                                                               ó,
                                                                       Score 18; DB 3; Length 18; Pred. No. 43;
                                                                                                             Indels
syndrome and the formation of atherosclerotic plaque
                                     Sequence 18 BP; 6 A; 4 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 15; SEQ ID NO 36; 135pp; English.
                                                         90.0%; Sc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dobie KW;
                                                                                                                                                                             1 CTTTCACCAAATTGGAAG 18
                                                                                                                                                   2 CTTTCACCAAATTGGAAG 19
                                                                                                                                                                                                                                                                                     ADI80035 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2002; 2002US-00189267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2002; 2002US-00189267
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                         Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-081742/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2004006030-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monia BP,
                                                                                                                                                                                                                                                                                                                          ADI80035;
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The invention relates to a novel antisense compound of 8-80 nucleobases

in length targeted to, and which specifically hybridizes with, a nucleic

acid molecule encoding transforming growth factor (TGP)-beta 2, and

inhibits the expression of TGP-beta 2. The invention further relates to:

a compound 8-80 nucleobases in length that specifically hybridizes with

a tleast an 8-nucleobase portion of an active site on a nucleic acid

molecule encoding TGF-beta 2; a composition comprising the compound and

carrier or diluent; inhibiting the expression of TGF-beta 2 in cells or

tissues by contacting the cells or tissues with the compound as the expression of TGF-beta 2 is inhibited; treating an animal having a

carrier or ordition associated with TGF-beta 2 by administering to the

carpression of TGF-beta 2 is inhibited; treating an antisense

compound. The antisense compound has cytostatic, nootropic,

neuroprotective, and immunosuppressive activities. The compound,

composition and methods are useful for treating a disease or condition

cancer, a neurodegenerative disorder, and alsease or condition

cancer, a neurodegenerative disorder, and alsease or condition

cancer, a neurodegenerative disorder, and alsease or condition
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                                                                                                                                                                                                                                                                                                                                      Human transforming growth factor-beta 2 target DNA region, SEQ ID No 182
                                                                                                                                                                                                                                                                                                                                                                           antisense; transforming growth factor; TGF, beta 2; TGF-beta 2; cytostatic; nootropic; neuroprotective; immunosuppressive; hyperproliferative disorder; cancer; neurodegenerative; hyperactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hyperactivation of an immune response. This polynucleotide sequence represents a preferred target DNA region of TGF-beta 2 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding TGF-beta 2, useful for treating cancer, a neurodegenerative disorder, or a disease involving hyperactivation of
                                       Gaps
                                     ;
0
                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 16; SEQ ID NO 182; 135pp; English.
90.0%; Score 18;
  90.00,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monia BP, Freier SM, Dobie KW;
                                                                             1 GCTTTCACCAAATTGGAA 18
                                                                                                              GCTTTCACCAAATTGGAA 20
                                                                                                                                                                                                                     踞
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2002; 2002US-00189267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2002; 2002US-00189267.
                                                                                                                                                                                                                     ADI80181 standard; DNA; 20
                                                                                                                                                                                                                                                                                                  (first entry)
                                     18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-081742/08.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              immune; ss; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004006030-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                  22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JAN-2004.
                                                                                                                                                                                                                                                           AD180181;
                                                                                                                                                                             RESULT 7
ADI80181/c
                                   Matches
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DB 12; Length 20; 44;

90.0%; Score 18; 100.0%; Pred. No.

Query Match Best Local Similarity

represents an antisense oligonucleotide of the invention.

Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

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This sequence is an immunosuppressant inhibitor oligonucleotide, which is used in the invention. The invention relates to a composition which used in the invention. The invention relates to a composition which contains at least one inhibitor (less than 100 kD) of a substance (e.g. transforming growth factor TGF-beta, vascular endothelial growth factor VEGF, interleukin-10 IL-10, prostaglandin B2 PGB2, or their receptors) that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. This colgonucleotide is an example of an inhibitor that is used in the composition. The composition is used as an immunostimulant for the composition. The composition is used as an immunostimulant for the composition. The composition is used as an immunostimulant for the composition. The composition is used as an immunostimulant for the composition. However, particularly hyperproliferation; levastance to neoplagms and infections, particularly hyperproliferation; colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours, malignant melanoma, brain tumours and sarcomas The oligonucleotides,
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                                                                                                                                                                                                                                                                                                                                                       Immunosuppressant inhibitor; transforming growth factor beta, TGF beta, vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer; prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative colitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or VEGF, are inhibitors of are useful as anti-
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatories for treating e.g. asthma, Crohn's disease, ulcerative colitis, diabetes, glomerulonephritis, acute respiratory distress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition containing immune stimulant and inhibitor of agent that adversely affects the immune response, for treating cancers and
    ö
                                                                                                                                                                                                                                                                                                                   Immunosuppressant inhibitor oligonculeotide TGF-beta2-14/3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.0%; Score 16; DB 3; Length 16; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 16; Conservative 0; Mismatches 0; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     syndrome and the formation of atherosclerotic plaque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              most of which are directed against TGFbeta or VEGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brysch W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlingensiepen R,
  ö
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                                          1 GCTTTCACCAAATTGGAA 18
                                                              18 GCTTTCACCAAATTGGAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Fig 1; 30pp; English.
                                                                                                                                                                                       AAZ65470 standard; DNA; 16 BP
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                                                                                                                                                                                                                                                                            (first entry)
18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlingensiepen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9963975-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-1999;
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                                                                                                                                                                                                                                                                            30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infections.
                                                                                                                                                                                                                                  AAZ65470;
Matches
                                                                                                                                                RESULT 8
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The antisense oligonucleotides are useful in the treatment of tumours in which expression of TGF-beta is of relevance for pathogenicity and/or inhibition of pathological angiogenesis. They are used especially for the treatment of the immunosuppressive effect of TGF-beta, augmentation of the proliferation of cytotoxic lymphocytes, treatment of endogenous hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas and malignant gliomas, including glioblastomas, treatment and prophylaxis of skin carcinogenesis, and treatment of oesophageal and gastric carcinomas. See AAQ78352-Q78488 The sequences given in GENESEQ files AAQ78352-Q78408 are antisenes oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
                                                                                                                                                                                                                                     Transforming growth factor beta; TGF-beta; antisense; treatment; tumour; angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma; carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut; immunosuppression; oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlingensiepen R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transforming growth factor beta anti:sense oligo:nucleotide(8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16; DB 2; Length 18; Pred. No. 4.4e+02;
                                                                                                                                                                                                            TGF-beta gene phosphorothioate antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analogues. (Updated on 25-MAR-2003 to correct PN field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlingensiepen G, Brysch W, Schlingensiepen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating immunosuppression, tumours, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.00
100.08; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 46; 74pp; English.
                                                                                                      AAQ78430 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                94WO-EP001362.
20
                           16
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93EP-00107849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
               1 TCACCAAATTGGAAGC
                                                                                                                                                                 (revised)
(first entry)
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5 TCACCAAATTGGAAGC
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-358266/44.
                                                                                                                                                                                                                                                                                                                                                                                                                29-APR-1994;
                                                                                                                                                                                                                                                                                                                                                   WO9425588-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-1993;
13-MAY-1993;
                                                                                                                                                               25-MAR-2003
27-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bogdahn U;
                                                                                                                                    AAQ78430;
                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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AAZ65453
ID AAZ65
XX
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                                                                         RESULT 9
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AAZ65453 standard; DNA; 18 BP

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0; Gaps

AAZ65453

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The invention relates to a pharmaceutical composition (PC) comprising one or more stimulators that stimulate the function of immune system and/or immune cells and one or more substances inhibiting cell proliferation and/or inducing cell death. A pharmaceutical composition is useful for treating neoplasms chosen from solid tumors; blood born tumors such as leukemias; cutte or chronic myelotic or lymphoblastic leukemia; tumor metastasis; benign tumors; or is chosen from bile duct carcinoma, bladder carcinoma, brain tumor, breast carcinoma, bronchogenic carcinoma, embryonal carcinoma, epithelial carcinoma, esophageal carcinoma, embryonal carcinoma, colon carcinoma, esophageal carcinoma, cervical carcinoma, colon carcinoma, agentic carcinoma, head and neck carcinoma, liver carcinoma, lung carcinoma, medillary carcinoma, non-small cell bronchogenic/lung carcinoma, ovarian carcinoma, pancreas carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pharmaceutical composition useful for treating neoplasm, comprises stimulators stimulating function of immune system and/or immune cells and substances inhibiting cell proliferation and/or inducing cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carcinoma, sebaceous gland carcinoma, testicular carcinoma, uterine carcinoma, rheumatoid arthritis and psoriasis. The present sequence represents a TGF-beta 2 inhibition oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      papillary carcinoma, papillary adenocarcinoma, prostate carcinoma, intestine carcinoma, rectal carcinoma, renal cell carcinoma, skin carcinoma, small-cell bronchogenic/lung carcinoma, squamous cell
                                                                                                   pharmaceutical; cell death; neoplasm; ss; Cytostatic; Apoptotic;
Immunostimulant; Antiarthritic; Antirheumatic; Antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 16; DB 14; Length 18; 100.0%; Pred. No. 4.4e+02; tive 0; Mismatches 0; Indels
                                                 TGF-beta 2 inhibition oligonucleotide SEQ ID NO 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 7 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schlingensiepen K, Schlingensiepen R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 34; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ANTI-) ANTISENSE PHARMA GMBH
                                                                                                                                                                                                                                                                                                                                                                          20-DEC-2004; 2004WO-EP053604.
                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2003; 2003EP-00029367.
05-FEB-2004; 2004US-0541771P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 TCACCAAATTGGAAGC 20
                                                                                                                                                             TGF-beta antagonist; Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ65469 standard; DNA; 15
08-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCACCAAATTGGAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-479334/48
                                                                                                                                                                                                                                                                 WO2005059133-A2.
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                                                                                                                                                                                                                                                                                                                     30-JUN-2005.
                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used in the invention. The invention relates to a composition which contains at least one inhibitor (less than 100 kD) of a substance (e.g. transforming growth factor TGF-beta, vascular endothelial growth factor YGGF, interleukin-10 LL-10, prostaglandin E2 PGBZ, or their receptors) that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. This oligonucleotide is an example of an inhibitor that is used in the composition. The composition is used as an immunostimulant for the treatment of neoplasms and infections, particularly hyperproliferation; leukaemia, (non-)Hodgkin's lymphoma, cardinoma (of oesophagus, bronch), colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumours, malignant melanoma, brain tumours and sarcomas. The oligonucleotides, money of which are directed against TGFbeta or VEGF, are inhibitors of
                                                                                                                                                     Immunosuppressant inhibitor; transforming growth factor beta; TGF beta; vascular endothalial growth factor; VEGF; interleukin-10; IL-10; cancer; prostaglandin E2; pGE2; immune response; tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative collitis; diabetes; glomerulonephritis; acute respiratory distress syndrome; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is an immunosuppressant inhibitor oligonucleotide, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatories for treating e.g. asthma, Crohn's disease, ulcerative colitis, diabetes, glomerulonephritis, acute respiratory distress syndrome and the formation of atherosclerotic plaque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%; Score 16; DB 3; Length 18; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels
                                                                                                         Immunosuppressant inhibitor oligonucleotide TGF-beta2-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brysch W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlingensiepen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0%; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98EP-00110709
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                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-097470/08
                                                                                                                                                                                                                                                                                               atherosclerosis
                                                                                                                                                                                                                                                                                                                                                   Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                     WO9963975-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-1998;
                                                       30-MAR-2000
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infections.

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Gaps

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Query Match Best Local Si Matches 16,

AEB01190;

SAXA

RESULT 11 AEB01190

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Immunosuppressant inhibitor oligonculeotide TGF-beta2-14/2.

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used in the invention. The invention relates to a composition which contains at least one inhibitor (less than 100 kD) of a substance (e.g. transforming growth factor TGF-beta, vascular endothelial growth factor VEGF, interleukin-10 IL-10, prostaglandin E2 PGEZ, or their receptors) that adversely affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. The composition also includes at least one stimulant that positively affects the immune response. This oligonucleotide is an example of an inhibitor that is used in the composition. The composition is used as an immunostimulant for the creatment of neoplasms and infections, particularly hyperproliferation, leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of cesophagus, bronchi, colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus, breast, ovary, cervix, endometrium, prostate or bladder), liver tumnorrs, malignant melanoma, brain tumours and sarcomas. The oligonucleotides, most of which are directed against TGFbeta or VEGF, are inhibitors of inflammatories for treating e.g. asthma, Crohn's disease, ulcerative collitis, diabetes, glomerullonephritis, acute respiratory distress syndrome and the formation of atherosclerotic plaque
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Immunosuppressant inhibitor; transforming growth factor beta; TGF beta; vascular endothelial growth factor; VGGF; interleukin-10; IL-10; cancer; prostaglandin E2; pGG2; immune response; tumour; asthma; Crohn's disease; monocyte chemotactic protein-1; MCP-1; ulcerative colltis; diabetes; glomerulonephritis; acute respiratory distress syndrome; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lysozyme gene expression control region, chromosomal positional effect, transgene; avian cell; PCR; primer; chicken; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition containing immune stimulant and inhibitor of agent that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence is an immunosuppressant inhibitor oligonucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adversely affects the immune response, for treating cancers and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken lysozyme gene fragment sequencing PCR primer, lys056for.
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Pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 6 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                     (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
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100.0%; Pred. No. ...
0; Mismatches
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nes 15; Conservative
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                                                                                                   atherosclerosis
                                                                                                                                                                           W09963975-A2
                                                                                                                                     Unidentified
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AAD48552/c
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molecule comprising an isolated avian lysozyme gene expression control region operably linked to a nucleic acid insert encoding a polypeptide. The nucleic acid is useful for reducing the chromosomal positional effect of a transgene operably linked to the lysozyme gene expression control region and transfected into a recipient avian cell. The present sequence is a PCR primer used for sequencing chicken lysozyme gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; 8s.
                                                                                                                                                                                                                                                                                                     invention relates to an isolated or recombinant nucleic acid or DNA
                                                                                                                                                                                                                   positional effect of a transgene, comprises an isolated avian lysozyme gene expression control region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric phosphorothioate oligonucleotide to target Navl.3 #5782
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.2; DB 8;
Pred. No. 3.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                            Example 1; Fig 1; 88pp; English
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                                                                                                     30-MAR-2001; 2001US-0280004P.
03-AUG-2001; 2001US-00922549.
25-JAN-2002; 2002US-0351550P.
                                                                              29-MAR-2002; 2002WO-US009866.
                                                                                                                                                                                                                                                                                                                                                                                                                                  71.0%;
84.2%;
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                                                                                                                                                      (AVIG-) AVIGENICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                      WPI; 2003-046807/04.
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                                WO200279447-A2
                                                                                                                                                                                                                                                                                                                                                                                        control region
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                                                        10-OCT-2002
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           Gallus
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ADK78448/c
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nucleic acid molecule encoding Nav1.3, where the antisense compound

WPI; 2004-203785/19

Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; ss. Chimeric phosphorothioate oligonucleotide to target Nav1.3 #5863. 1 GCTTTCACCAAATTGGAAG 19 19 GCTTCCAGCAAATGGGAAG 1 ADK78529 standard; DNA; 20 BP. 14-AUG-2003; 2003WO-US025465 14-AUG-2002; 2002US-0403416P 20-MAY-2004 (first entry) Query Match
Best Local Similarity 84.2' (PHAA) PHARMACIA CORP WPI; 2004-203785/19. WO2004016754-A2. 26-FEB-2004. Roberds SL; Synthetic. ADK78529; RESULT 15 ð 셤

Navl.3, useful for useful for treating a disease or condition associated with Navl.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.

The present invention relates to an antisense compound targeted to

Claim 4; SEQ ID NO 5863; 417pp; English.

New antisense compound targeted to a nucleic acid molecule encoding

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Gaps

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specifically hybridizes with and inhibits the expression of Navi.3. The compound and composition are useful for treating a disease or condition associated with Navi.3. e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate headache; seizure disorder such as childhood seizure disorder including but not limited to neonatal or infantile epilepsy; or ataxia. The present sequence represents a chimeric phosphorothioare oligonucleotide with human Navi.3 expression, the oligonucleotides are designed to target different regions of the human Navi.3 RNA. Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other; Query Match Matches ð 셤 nucleic acid molecule encoding Navi.3, where the antisense compound specifically hybridizes with and inhibits the expression of Navi.3. The compound and composition are useful for treating a disease or condition associated with Navi.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, diabetic neuropathy, trigeminal neuropathy, arthritic pain, lower back pain, pain from burns, migraine headache, cluster headache, mild-to-moderate headache; seizure disorder such as childhood seizure disorder, including but not limited to neonatal or infantile epilepsy; or ataxia. The present sequence represents a chimeric phosphorothhoate oligomucleotide with 2'MOE wings and a deoxy gap. Used during the antisense inhibition of human Navi.3 expression, the oligomucleotides are designed to target New antisense compound targeted to a nucleic acid molecule encoding Navl.3, useful for useful for treating a disease or condition associated with Navl.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia. The present invention relates to an antisense compound targeted to a 71.0%; Score 14.2; DB 12; Length 20; 84.2%; Pred. No. 3.6e+03; Live 0; Mismatches 3; Indels (Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other; Claim 4; SEQ ID NO 5782; 417pp; English.

ö Gaps ö 71.0%; Score 14.2; DB 12; Length 20; 84.2%; Pred. No. 3.6e+03; Indels 0; Mismatches Search completed: March 4, 2006, 02:31:42 Job time : 393.947 secs 1 GCTTTCACCAAATTGGAAG 19 20 GCTTCCAGCAAATGGGAAG 2 Local Similarity 84.2 hes 16; Conservative

us-09-701-583a-14.sz40.rst

Perfect score:

Sequence:

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OM nucleic

Run on:

Scoring table:

Searched:

Database

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BH792339 SALK_0640
BH905278 SALK_1058
CZ469111 C04246-5p
AL485473 T. brucei
CZ94724 SALK 0549
AZ309847 1M0017408
AZ309847 1M0017408
AZ30443 TLEAF--07
AZ761083 1M0555A13
AZ761083 1M0555A13
AZ7844054 ZM0173M19
CL528503 ASV17E05.
BH811021 SALK_0973
BH865074 SALK_0973
BH865074 SALK_0973
BH865074 SALK_0973
BH865074 SALK_0973
BH865079 AZ680091
AZ580321 AU259281
BH86509 CS24737-3p
AZ56801 1M0368022
AZ668401 1M0368022
                                                                                                                                                                                                                                                                                                                                                      EST 08-NOV-2001
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I (basea I to 34)
Satch, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Contact: Nori Satch
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cissue type="whole animal"
/dev stage="larva"
/clone_lib="Nori Satoh unpublished cDNA library, larva"
                                                                                                                                                                                                                                                                                                                                                     34 bp mRNA linear EST 08 4V952639 Nori Satoh unpublished cDNA library, larva Ciona Intestinalis cDNA clone rcilv19c08 3', mRNA sequence.
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Pred. No. 8e+04;
0; Mismatches 1; Indels
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Ciona intestinalis"
|mol_type="mknA"
|db_xref="taxon:719"
|clone="rcilv19c08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                             ALIGNMENTS
  BH792339
BH905278
CZ469111
TA285H02Q
                                                                               CF302443
AZ761083
AZ781725
AZ864054
CL528503
                                                                                                                                                     BH865074
AU259281
BH856768
AJ596091
CZ416273
AZ56091
CZ41273
AZ56401
CZ471370
                                                CC794724
AZ309847
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Ciona intestinalis
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Best Local Similarity 93.3
Matches 14; Conservative
    Kyoto University
    AV852639
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                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                               RESULT 1
AV852639/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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CG729682/c
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CR395105 Arabidops
AZ789746 ZM0037M14
CR358544 Arabidops
BH854633 KG06875-5
AI790036 ue66h11.r
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B2769257 SALK 1418
AZ336391 1M0066G07
BH863411 SALK 0938
AZ645914 1M0511K08
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BZ661352 SALK 0248
A1823627 wi85e02.x
AA887375 oj53908.s
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AU255583 AU255583
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                                                                               4, 2006, 01:46:27; Search time 3170.53 Seconds (without alignments) 295.138 Million cell updates/sec
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Biocceleration Ltd.
                                                                                                                                                                                                             41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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              GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                           Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           nucleic search, using sw model
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13.4 12.8 12.8 12.6 12.2 12.2 12.2

Result

11.8 11.9 11.9 11.0 11.0 11.6 11.6 11.6

18 119 22 22 υυ

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Gaps

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'clone="IMAGE:1646933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                       Tumor Gene Index
Unpublished (1997)
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BZ769257/c
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/clone lib="1119" - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHi; Site 2: BgLII; RescueMu is a 4.9 kb, modified maize Mu transposon dealigned to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastec.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BgIII, and ligated to form circular plasmids. DHIOB cells were transformed and then screened on LB plates with ampicillin."
25 bp DNA linear GSS 20-OCT-2003 1119114B03.2EL_Y1 1119 - RescueMu Grid AA Zea mays genomic, genomic CG729682
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                                                                                                                                                                                                                                                                                                  Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

    (bases 1 to 25)

                                                                                                                                                                                                                                                                                                                                                                     Department of Biological Sciences
Stanford University
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Pax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119114 row: B column: 03
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 25;
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87.5%; Pred. No. 1.5e+05;
iive 0; Mismatches 2;
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: transposon-tagged
                                                                                                                CG729682.1 GI:37771623
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Homo sapiens
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Best Local Similarity 87.5'
Matches 14; Conservative
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BZ769257 37.05.x Arabidopsis thaliana TDNA insertion lines Arabidopsis clone SALK_141859.37.05.x, genomic clone SALK_141859.37.05.x, genomic
                                                                                                                                                                                                                                                                            Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="parathyroid tumor"
/dev stage="adult"
/lab_host="bhlub"
/clone_lib="Soares_parathyroid tumor_NbHPA"
/clone_lib="Soares_parathyroid d_land; Vector: pT7T3D
/pharmacial with a modified polylinker; Site_l: Not I;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Sadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
1 (bases 1 to 31)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D.,
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome S
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                   Trace considered overall poor quality
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Arabidopsis thaliana
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BH863411.1 GI:22099002
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Unpublished (2001)
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Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Roose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                    This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g35820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%; Score 12.6; DB 9; Length 33; 78.9%; Pred. No. 2e+05; ive 0; Mismatches 4; Indels
                                    Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 558 518 6379
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                    'organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0066 row: G column: 07
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                        /mol_type="genomic_DNA"
/ecotype="Col-0"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                            db_xref="taxon:3702"
                                                                                                                                                                                          Class: TDNA tagged.
Location/Qualifiers
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                    Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCTTTCACCAAATTGGAAG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 78.9
Matches 15; Conservative
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  Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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DEFINITION
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp42 (gilfy12114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Farker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                  lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
11:1: 858 453 4100 x1752
Fax: 858 558 6379
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/mol_type="genomic DNA"
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/clone="UUGC1M0066G07"
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Location/Qualifiers
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Query Match
Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Rummalia; Butheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Murinae; Mus.

1 (bases 1 to 34)

S Dunn, D., Aoyagai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid innearts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ645914 1inear GSS 14-DEC-2000 1M0511K08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0511K08 R, genomic survey sequence.
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/clone="SALK_093836"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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                                                                                                                                                                                                                                                                     Query Match 61.0%; Score 12.2; DB 9; Length 26; Best Local Similarity 82.4%; Pred. No. 3.1e+05; Matches 14; Conservative 0; Mismatches 3; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: K column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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ferrain="C57BL/6J"
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/clone="UUGCIMO511K08"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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Location/Qualifiers
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GSS.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Murcidea; Murinae; Mus.

1 (bases 1 to 21)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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21 bp DNA linear GSS 29-SEP-2000
1M0010J17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0010J17 R, genomic survey sequence.
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/clone llb="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/GJ (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: J column: 17
Seg primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
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Location/Qualifiers
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Mus musculus
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Fax: 801 585 7177
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BH904979 11.05414.53.00.x Arabidopsis thaliana TDNA insertion lines Arabidopsis clone SALK 105414.53.00.x, genomic clone SALK 105414.53.00.x, genomic
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Alonso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J. R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/clone lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 659 679 Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (thale cress)
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     GGTTTCACCAGATTTAATGC 7
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Unpublished (2001)
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Best Local Similarity
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarase gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114|gb|AR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, TE1:82-42-866-7181, Fax:82-42-66-4409) Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS 06-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Bun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. Direct Submission
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Pan troglodytes DNA, clone: RP43-090L01.T7, genomic survey
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/clone_lib="RP-43 Chimpanzee Male_BAC_Library"
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75.0%; Pred. No. 3.9e+05;
iive 0; Mismatches 5;
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mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-090L01.T7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Pan troglodytes
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R.Site 1 : ECORI
R.Site 2 : ECORI.
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AG204809.1 GI:45236984
GSS.
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Best Local Similarity 75.0
Matches 15; Conservative
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Matches 12; Conservative
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AJ600156 32 15-JAN-2004 Arabidopsis thaliana T-DNA flanking sequence, right border, clone
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                                               Gaps
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Length 32;
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GSS, right border, T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Score 12; DB 9;
Pred. No. 4e+05;
                                           0; Mismatches
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Gaps

1 GCTTTCACCAAATTGGAAGC 20

us-09-701-583a-14.sz40.rst

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1. 31

Organism="Mus musculus"

/mol_type="mRNA"

/db Xref="taxon:10090"

/clone="BED0005815"
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Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue gaston Cremieux, 91057 Evry cedex, FRANCE
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has program Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers
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BED0005815 3', mRNA sequence.
                                            Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Ahauvin, S., Bechlold, N., Craud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
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1 (bases 1 to 31)

Kato, K. and Matoba, R.
Generation of expressed sequence tags from mouse brain unpublished (2002)
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  cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkaro@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Arabidopsis thaliana"
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1. .3
1. .52 - T-DNA flanking sequence
right border"
                                                                                                                                      of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
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/db_xref="taxon:3702"
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/clone lib="MPDIX-ADIS-024-leaf"
/clone lib="Wetcor: pCMVSPORT6; Site 1: Sall; Site 2: Notl;
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Notl;
Containwantlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Notl, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bikaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bikaryota; Viridiplantae; Streptophyta; Garyophyla; Garyophylalaes, Magnoliophyta; eudicotyledons; Caryophylalaes, Amaranthaceae, Beta.

1 (bases 1 to 32)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., and Radelof, U. Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQS87054 11n-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-011-H11 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                             Gaps
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                                                                                                                              Length 31;
tissue type="brain"
/clone_lib="3'-directed mouse cDNA library"
                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: Weisshaa@mpiz-koeln.mpg.de
Insert Length: 32 Std Error: 0.00
Plate: 11 row: H column: 11
Seq primer: SP6; CATACGATTTAGGTGCACTATAG.
                                                                                                                          59.0%; Score 11.8; DB 1; 86.7%; Pred. No. 5e+05; tive 0; Mismatches 2;
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/organism="Beta vulgaris"
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/db_xref="taxon:161934"
/clone="024-011-H11"
/tissue_type="leaf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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us-09-701-583a-14.sz40.rst

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/mol_type="miNNA"
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/note="Grgan: kidney; Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Bco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clone1Ds 132912-1325811, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                            Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                              Hominidae, Homo.

1 (bases 1 to 37)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Gancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
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Pred. No. 5.1e+05;
0; Mismatches 2;
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/organism="Homo sapiens"
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Location/Qualifiers
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Seg primer: -40UP from Gibco
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86.7%;
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                        Homo sapiens (human)
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Best Local Similarity 86.7
Matches 13; Conservative
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Job time: 3174.53 secs
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                      SOURCE
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AUTHORS
TITLE
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A1823627.1 GI:54444298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Arabidopsis thaliana TDNA insertion lines" /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                       This is single pass sequence recovered from the left border of NINA. This sequence lies within an annotated exon of At2g17360.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyle
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute Genomic Analysis Laboratory (SIGnAL) 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 958 558 6379 Email: ecker@salk.edu
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                                              Indels
Pred. No. 5.1e+05;

    .36
    /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"

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                                            0; Mismatches
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BZ661352.1 GI:28174499
                   86.78;
                                                                                          2 CTTTCACCAAATTGG 16
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                                                                                                                          23 CTTTCACTATATTGG 9
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                      Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity
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Length 37; Indels

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Sequence 40, Appl Sequence 58, Appl Sequence 39, Appl

Sequence Sequence S

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Appl 196,

Sequence Sequence 1

Sequence

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Sequence Sequence Sequence Sequence

Sequence

US-09-396-196G-127149 US-09-396-196G-18089

ALIGNMENTS

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APPLICANT: Schlingensiepen, Georg-Ferdinand
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Rarl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
NUMBER OF SEQUENCES: 137
US-09-396-196G-40788

US-09-396-196G-62362

US-09-396-196G-81442

US-09-396-196G-81444

US-09-396-196G-81444

US-09-396-196G-81444

US-09-012-097A-40

US-09-481-620A-58

US-09-481-620A-58

US-09-589-470-6

US-09-589-470-6

US-09-589-470-6

US-09-231-0770-2

US-09-231-0770-2

US-09-396-196G-9647

US-09-396-196G-9647

US-09-396-196G-3788

US-09-396-196G-13788

US-09-396-196G-13788

US-09-396-196G-13788

US-09-396-196G-1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 2004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ER PLOPPY disk
COMPUTER: FORMS: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-666
TELEPAX: (202)393-5350
TELEFAX: (202)393-5350
TELEFAX: (202)393-5350
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
PILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 849.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 79, Application US/08535249
Patent No. 6455689
GENERAL INFORMATION:
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TYPE: nucleic acid
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ADDRESSEE: Jacobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic
STRANDEDNESS:
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122784,
                                                                                                                                   March 4, 2006, 01:49:32 ; Search time 76.8421 Seconds (without alignments) 462.653 Million cell updates/sec
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                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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ptodata/1/ina/PTUS.cOMB.seq:*
ptodata/1/ina/PP_COMB.seq:*
ptodata/1/ina/RE_COMB.seq:*
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ptodata/1/ina/6A_COMB.seq:*/ptodata/1/ina/6B_COMB.seq:*
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US-09-396-196G-71642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-696-791-4062
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                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-118-387-4
-08-306-871-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-293-854-12
                                                                                                                                                                                                                                                                                                                                                                1303057 seqs, 888780828 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                                                                  gctttcaccaaattggaagc 20
                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                  US-09-701-583A-14
20
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Match Length
                                                                                                                                                                                                                                                                                                        IDENTITY NUC
                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
•MaxdmumrDBRsegglength: 402
                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                 OM nucleic
                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                                         Run on:
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No.
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Length 29;

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66.0%;
69.04;
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Query Match
Best Local Similarity 78.99
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)227-594
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: BOSTON
STATE: MASSACHUCETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                            US-08-465-590-42
                                                                                                                                                                                                                                                                                          RESULT 4
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Patent No. 6525185

GENERAL INFORMATION:
APPLICANT: Fan, Jian Bing
APPLICANT: Chakravarti, Aravinda
APPLICANT: Halushka, Marc Kenneth
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Polymorphisms Associated With
TITLE OF INVENTION: Hypertension
FILE REFERENCE: 018547-034210US
CURRENT FILING DATE: 1999-05-03
EARLIER APPLICATION NUMBER: US 60/084,641
EARLIER APPLICATION NUMBER: US 60/084,641
EARLIER PELING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 909
SOFTWARE FRANCE: FRANCE FR
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84.2%; Pred. No. 5.6e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                               DB 3; Length 18;
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JOS-029-03-1906-0827

PREPAIR OF 6827-24

GENERAL INFORMATION:

APPLICANT: Michael Mittmann

APPLICANT: David Mack

APPLICANT: David Mack

APPLICANT: David Mack

APPLICANT: David Mack

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 310.1.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT PILING DATE: 1999-09-15

PRIOR PILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FRAELSEQ for Windows Version 4.0

SEQ ID NO 6827
                                                                                                                                                         Query Match

80.0%; Score 16; DB

Best Local Similarity 100.0%; Pred. No. 60;

Matches 16; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTCAGCAAGTTAGAAGC 23
                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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US-09-304-232-470
                                                                                                                                                                                                                                                                                          5 TCACCAAATTGGAAGC 20
                                                                                                                                                                                                                                                                                                                                                          1 TCACCAAATTGGAAGC 16
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Matches 16; Conservative
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      unknown
                                                                                                                                                            Query Match
Best Local Similarity
                                 MOLECULE TYPE: I
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US-09-304-232-470/c
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US-09-396-196G-6827
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                                                               , ANTI-SENSE:
US-08-535-249-79
      TOPOLOGY:
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LENGTH: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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US-08-711-417C-42
is Sequence 42, Application US/08711417C
j Batent No. 6228611
j GENERAL INPORMATION:
j GENERAL INPORMATION:
j APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
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                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Georgopoulos, Katia A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 24;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
Score 13.8; DB 3;
Pred. No. 9.2e+02;
1; Mismatches 3;
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Pred. No. 1.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-UN-1995
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1993
FILING DATE: 14-SEP-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                          Sequence 42, Application US/08465590 Patent No. 5824770
                                                                                        1 GCTTTCACCAAATTGGAAG 19
                                                                                                                                 25 GTTTTCACCCWGTTGGAAG 7
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Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.2; DB 3;
Pred. No. 1.8e+03;
                                                                                                                                                                                                                 NAME: Myers, Louis P.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.8e
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-723-909-42
                                                            APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
                                                                                                                                                APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application PC/TUS9308743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 946,233
                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 24 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.0%;
83.3%;
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
    PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
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APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                TELEX: 200154
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Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6630141
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SEPLICANT:
GEOGROULOS, KATIA A.
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
NUMBER OF SEQUENCES: 202
CORRESPONDENCE ADDRESS:
ADDRESSES: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.0%; Score 13.2; DB 3; Length 24; 83.3%; Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,417C
FILING DATE: 05-5ep-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: Windows 95 SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Myers, Louis P.
RRGISTRATION UNDMER: 35,965
REFERENCE/DOCKET NUMBER: 10287/007001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/723,909
FILING DATE: 28-No. 6630141-2000
                                          ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/238,212
FILING DATE: 02-MAY-1994
PAPLICATION NUMBER: 08/121,438
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: 07/946,233
FILING DATE: 14-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 225 Franklin Street
                                                               STREET: 225 Franklin Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09723909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TTTCACCAAATTGGAAGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 42:
NUMBER OF SEQUENCES: 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                            COUNTRY: USA
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Best Local Similarity
Matches 15; Conserv
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US-09-723-909-42
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FILE REFERENCE: 480124.407
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4163
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 71637, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCTTTCACCAAATTGG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: mus musculus US-09-396-196G-71637
                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-396-196G-71637
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Sequence 4062, Application US/09696791

Sequence 4062, Application US/09696791

GENERAL INFORMATION:

APPLICANT: Robbins, Joan M.

APPLICANT: Tritz, Richard

TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE

TITLE OF INVENTION: SKIN AND EYE DISEASES

FILE REPREMENT S. 49024.407

CURRENT APPLICATION NUMBER: US/09/696,791

CURRENT FILING DATE: 2000-10-25

NUMBER OF SEQ ID NOS: 4523

SOFTWARE: PALENTIN Ver. 2.0

SEQ ID NO 4062

LENGTH: 19
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PREMENT 0. 6770633

GRNERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Tritz, Richard
ITTLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
ITTLE OF INVENTION: SKIN AND EYE DISEASES
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Best Local Similarity 87.5%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.0%; Score 13.2; DB 3; Length 25; Best Local Similarity 83.3%; Pred. No. 1.9e+03; Matches 15; Conservative 0; Mismatches 3; Indels
                                                                 Sequence 122784, Application US/09396196G
Facence 122784, Application US/09396196G
Facence 122784, Application US/09396196G
Facence 122784, Application US/09396196G
FAPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1998-09-15
FRICR APPLICATION NUMBER: 60/100,678
FRICR APPLICATION NUMBER: 60/100,678
FRICR APPLICATION NUMBER: 60/100,678
FRICR SEQ ID NOS: 127866
SOFTWARE: FeatsBQ for Windows Version 4.0
SEQ ID NO 122784
INDER THE SECTION NUMBER: MINDER THE SECTION NUMBER OF SEQ ID NO 122784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-4062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TTTCACCAAATTGGAAGC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: mus musculus
US-09-396-196G-122784
                           RESULT 8
US-09-396-196G-122784
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US-09-696-791-4062/c
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Gaps
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                                                                    Length 19;
                                                                                                                  Indels
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US-09-396-71638
i Sequence 71638, Application US/09396196G
i Patent No. 6821724
i GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 310.1.
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71638
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: David Lockhart
TICLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71637
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64.0%; Score 12.8; DB 3;
Best Local Similarity 87.5%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 2;
                                                                 Query Match
64.0%; Score 12.8; DB 3;
Best Local Similarity 87.5%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 2;
) OTHER INFORMATION: PCNA HH ribozyme binding site US-09-696-791-4063
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                                                                                    Query Match 64.0%; Score 12.8; DB 3; Length 25; Best Local Similarity 87.5%; Pred. No. 3e+03; Matches 14; Conservative 0; Mismatches 2; Indels
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3e+03;
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                                                                                                                                                                                                                                                                                   RESULT 13
US-09-396-196G-71639
; Sequence 71639, Application US/09396196G
; Patent No. 6821724;
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-396-196G-71640
Sequence 71640 Application US/09396196G
Sequence 71640 Application US/09396196G
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: AFFINEX: Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
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CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION UNDHER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71640
LENGTH: 25
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Best Local Similarity 87.5%; Pred. No. 3e
Matches 14; Conservative 0; Mismatche
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CURRENT FILING DATE: 1,999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                         8 GCTGTCACCAATTTGG 23
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: mus musculus
US-09-396-196G-71640
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US-09-396-196G-71639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 3101.1
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LENGTH: 25
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1 GCTTTCACCAAATTGG 16

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Gaps
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                                                                                                                                                                                                 APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymerrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: PascSEQ For Windows Version 4.0
SEQ ID NO 71641
                                                                                                                    ; Sequence 71641, Application US/09396196G; Patent No. 6821724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: March 4, 2006, 02:07:26 Job time: 77.8421 secs
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4 GCTGTCACCAATTTGG 19
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                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Michael Mittmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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RESULT 2
US-11-121-849-447577/C
US-11-121-849-447577/C
US-11-121-849-447577/C
US-11-121-849-447577/C
US-11-121-849-447577/C
Sequence 447577/A Application US/11121849
Sequence 447577/A Paplication No. US-20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded:
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: John Palma Title OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays FILE REFERENCE: 3684.1 CURRENT APPLICATION NUMBER: 2005-05-03 PRIOR APPLICATION NUMBER: 60/567,949 PRIOR APPLICATION NUMBER: 60/567,949 PRIOR FILING DATE: 2004-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 529681
LENCTH: 25
                 12 US-11-137-315A-19

12 US-11-121-849-429730

12 US-11-121-849-431099

12 US-11-121-849-515908

12 US-11-121-849-673778

12 US-11-121-849-673779

12 US-11-136-527-309345

12 US-11-136-527-309345

12 US-11-136-527-309363

12 US-11-136-527-309363

12 US-11-136-527-309372

12 US-11-136-527-309372

13 US-11-121-849-11860

14 US-11-121-849-118160

15 US-11-121-849-118160

17 US-11-121-849-1052

18 US-11-121-849-1052

19 US-11-121-849-206299

10 US-11-121-849-206599

11 US-11-121-849-206599

12 US-11-121-849-206599

13 US-11-121-849-206599

14 US-11-121-849-206599

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16 US-11-121-849-20659
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Pred. No. 1e+02;
0; Mismatches 1;
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Publication No. US20050272080A1
GENERAL INFORMATION:
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapien
US-11-121-849-529681
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Sequence 345854,
Sequence 673774,
Sequence 673775,
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Sequence 278180,
Sequence 634116,
Sequence 323453,
Sequence 206297,
Sequence 206297,
Sequence 206856,
Sequence 1091627,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                         March 4, 2006, 01:58:42; Search time 495.789 Seconds (without alignments) 88.444 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Cgn2_6/ptodata/1/pubpna/USOB NEW PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USOB_NEW PUB.seq:*
                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 US-11-121-849-529681
2 US-11-131-849-447577
2 US-11-136-527-28180
2 US-11-121-849-634116
2 US-11-121-849-533434
2 US-11-121-849-206298
2 US-11-121-849-206298
2 US-11-121-849-206855
2 US-11-121-849-206855
2 US-11-121-849-206855
2 US-11-121-849-673774
2 US-11-121-849-673775
2 US-11-121-849-673775
2 US-11-121-849-673775
3 US-11-121-849-673775
2 US-11-121-849-673776
3 US-11-121-849-673777
1 US-11-101-244-1430638
1 US-11-01-344-1430638
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                                                                                                                    OM nucleic - nucleic search, using sw model
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Match Length
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Gaps

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Indels

Result No.

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Sequence 673776, Sequence 673777, Sequence 1430638, Sequence 1430638, Sequence 791928,

Sequence 905217, Sequence 192, App Sequence 118160, Sequence 206299, Sequence 206858, Sequence 206858,

Sequence

Sequence 309345, Sequence 309363, Sequence 309371, Sequence 309372, Sequence 1149636, Sequence 1149636,

Sequence 4 Sequence 5 Sequence 6

Sequence

Sequence

Sequence

Sequence

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US-1121-849-583444

i Sequence 583444, Application US/11121849

i Sequence 583444, Application US/11121849

i Publication No. US20050272080A1

i Publication No. US20050272080A1

i RENERAL HORMATION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S.

i TITLE OF INVENTION: Microarrays

i TITLE OF INVENTION: Microarrays

i TITLE OF INVENTION: 1004-05-03

i CURRENT FILING DATE: 2005-05-03

i RICR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

i NUMBER OF SEQ ID NOS: 673904

is SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Publication No. US20050272080A1
GENERAL INFORMATION:
A PAPLICANT: JOHN Palma
1 TITLE OF INVENTION:
TITLE OF INVENTION: Microarrays
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Pred. No. 6.2e+02;
0; Mismatches 2;
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Pred. No. 9.7e+02;
5; Mismatches 1;
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Best Local Similarity 88.9%;
Matches 16; Conservative
                   TTTCACCAAATTGGA 17
                                                     15 Trrcaccaaarreda 1
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Best Local Similarity 62.5'
Matches 10; Conservative
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US-11-121-849-583444
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; Publication No. US20050272080A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded & TITLE OF INVENTION: Microarrays
FRIOR PILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 634116
LENGTH. 25
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Bublication No. US20050287570A1

Publication No. US20050287570A1

Publication No. US20050287570A1

APPLICANT: Wyeth

APPLICANT: Mounts, William M

TITLE OF INVERTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PILING DATE: 2005-05-06
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NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 447577
LENGTH: 25
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85.0%; Pred. No. 3.9e+02;
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Pred. No. 3.9e+02;
0; Mismatches 3;
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                                                                                                                                                                                        0; Mismatches
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SOFTWARE: Patentin version 3.2
SEQ ID NO 278180
LENCTH: 25
                                                                                                                                                   Query Match 76.0%
Best Local Similarity 85.0%
Matches 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.03
Matches 17; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Probe US-11-136-527-278180
                                                                           ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-447577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapien
US-11-121-849-634116
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US-11-121-849-634116/c
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US-11-136-527-278180
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GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded & TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded & TITLE OF INVENTION: Microarrays
FILE REPERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2006-05-03
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Beltwich, Isaac
APPLICANT: Shiler, Kuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06097.0200.0200.0200.0000
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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                          Length 25;
                       Score 14.4; DB 12;
Pred. No. 9.8e+02;
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Pred. No. 1.2e+03;
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                                                                  Mismatches
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Pred. No. 9.8
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; Sequence 1191627, Application US/10310914A
; Publication No. US20060003322A1
                                                                                                                                                                                                                                                    US-11-121-849-206857/c
; Sequence 206857, Application US/11121849
; Publication No: US20050272080A1
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Publication No. US20050272080A1
                       72.0%;
93.8%;
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Best Local Similarity 93.8%;
Matches 15; Conservative
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SOFTWARE: PatentIn version 3.
                                                                                                                                                            17 TTTCACCAAATAGGAA
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                                                                    Conservative
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US-11-121-849-206857
Query Match
Best Local Similarity
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 206857
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded STILE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR PELING DATE: 2006-05-03
PRIOR PLING DATE: 2006-05-03
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR PELING DATE: 2006-05-03
PRIOR FILING DATE: 2004-05-03
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                                                                                                                                                                                                                                                                                                                         Length 25;
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 206856
LENGTH: 25
                                                                                                                                  NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 206297
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 206298
LENGTH: 25
                                                                                                                                                                                                                                                                                                                         72.0%; Score 14.4; DB 12;
93.8%; Pred. No. 9.8e+02;
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Publication No. US20050272080A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 206298, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
                                                                                       PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                       Query Match 72.0
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                  ORGANISM: Homo sapien
US-11-121-849-206297
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US-11-121-849-206298
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US-11-121-849-206856
                                                                       CURRENT FILING DATE:
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US-11-121-849-206856/c
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Length 25;

Score 14.2; DB 12; Pred. No. 1.2e+03;

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APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded & TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded & TITLE OF INVENTION: Microarrays
FILE REPERENCE: 3664.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR PRILICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 673775
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: March 4, 2006, 03:54:50 Job time: 497.289 secs
                                                                                                                                                                                                                                                                                                                              US-11-121-849-673775
; Sequence 673775, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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84.2%;
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Best Local Similarity 84.2%;
Matches 16; Conservative (
                                                               Query Match
Best Local Similarity 84.2<sup>3</sup>
Matches 16; Conservative
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; ORGANISM: Homo sapien
US-11-121-849-673775
; ORGANISM: Homo sapien
US-11-121-849-673774
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     TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SEQ THARRE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 191
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 345864, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Pelma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded:
TITLE OF INVENTION: Microarrays
FILE REPRENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 345854
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Sequence 673774, Application US/11121849

Publication No. US20050272080A1

GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR PRIOR PRILCATION NUMBER: 05/57,949
PRIOR PILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Pred. No. 1.2e+03;
0; Mismatches 3;
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71.0%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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/ ORGANISM: Homo sapien
US-11-121-849-345854
                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapien
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US-11-121-849-345854
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Length 25;

Score 14.2; DB 12; Pred. No. 1.2e+03; O. Mismatches 3;

Sequence 313402, Sequence 972, App Sequence 73, Appl Sequence 121933, Sequence 612371, Sequence 612371, Sequence 62123, Sequence 621123,

Sequence 789786

Sequence 415013 Sequence 492824 Sequence 13117

Sequence 63888, A Sequence 63903, A Sequence 260911, Sequence 262958,

Sequence 277348,

Sequence 6827, Ap. Sequence 862258, Sequence 873648, Sequence 940467,

OM nucleic

Run on:

Sequence:

Searched:

Database

Result

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Sequence 5, Application US/10220033
Publication No. US20030186906A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Raimar
APPLICANT: Schlingensiepen, Reimar
TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene
TITLE OF INVENTION: gene
FILE REFERENCE: P68119US0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: antisense;
CTHER INFORMATION: oligonucleotide
US-10-220-033-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-984-919-532
; Sequence 532, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTIENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/F63763USO
                          0 US-11-036-317-862258

0 US-11-036-317-862258

0 US-11-036-317-940467

0 US-11-060-756-63903

0 US-11-060-756-63903

0 US-11-060-756-63903

0 US-11-060-756-262958

0 US-11-060-756-22958

0 US-11-060-756-22958

US-10-719-956-313402

US-10-898-660-73

US-10-898-660-73

US-10-719-956-612371

US-10-719-956-623123

US-10-719-956-623123

US-10-719-900-415013

US-10-719-900-415013

US-10-719-900-415013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/220,033
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: PCT/EP01/02694
PRIOR FILING DATE: 2001-03-10
PRIOR APPLICATION NUMBER: EP00105190.3
PRIOR PILING DATE: 2000-03-11
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 20; Conservative
 JS-10-220-033-5
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LENGTH: 20
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Sequence 915488;
Sequence 986433,
Sequence 60, Appl
Sequence 60, Appl
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Sequence 532, App
Sequence 1273, App
Sequence 182, App
Sequence 1875, App
Sequence 1275, App
Sequence 79, App
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Sequence 862259,
Sequence 873649,
Sequence 940468,
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Sequence 1274, Ap
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Sequence 974400,
                                                                                                     4, 2006, 01:49:48; Search time 417.368 Seconds (without alignments) 396.263 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 585916,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
               5.1.7
Biocceleration Ltd.
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US-11-036-317-873649
US-11-036-317-940468
US-10-719-956-259831
US-10-984-919-1274
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US-10-681-773-103539
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US-10-114-739A-60
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                      9793542 seqs, 4134689005 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
             GenCore version
Copyright (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                                           nucleic search, using sw model
                                                                                                                                                                                                        gctttcaccaaattggaagc 20
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                       Scoring table:
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6; Length 20 Indels ö

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Sequence 1275, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Karl-Hermann
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; TITLE REPERBNCE: 10496/P63763USO
; CURRENT FILING DATE: 1099-01-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR PILING DATE: 1998-01-30
; PRIOR PILING DATE: 1998-01-30
; PRIOR PILING DATE: 1999-01-31
; PRIOR PILING DATE: 1999-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 182, Application US/10189267
Publication No. US20040006030a1
GENERAL INFORMATION:
APPLICANT: Breat P. Monia
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
FILE REFERENCE: PTS-0038
CURRENT APPLICATION NUMBER: US/10/189,267
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 284
SEQ ID NO 182
TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 6; Length 20;
Pred. No. 41;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                                                                                                              Query Match 90.0%; Score 18; DB 6; Best Local Similarity 100.0%; Pred. No. 41; Matches 18; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antisense Oligonucleotide US-10-189-267-36
                                               CURRENT APPLICATION NUMBER: US/10/189,267
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 284
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100.0%; Pre
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                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 18; Conservative
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SOFTWARE: Patentin Ver. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-189-267-182/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-984-919-1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-189-267-182
                                                                                                                                                          LENGTH: 20
                                                                                                                             SEQ ID NO 36
                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
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APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Brysch, Wolfgang
TITLE OF INVENTION: ANTIERNES OLIGONUCLEOTIDE PREPARATION METHOD
FILE REFERENCE: 10496/P63703USO
CURRENT APPLICATION NUMBER: US/10/984,919
CURRENT APPLICATION NUMBER: US/09/341,700
PRIOR APPLICATION NUMBER: DS/09.24
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-01-30
PRIOR FILING DATE: 1999-01-31
NUMBER OF SEQ ID NOS: 1764
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1273
LENGTH: 18
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Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 18; 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.0%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 40; Matches 18; Conservative 0; Mismatches
                  CURRENT FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US/09/341,700
PRIOR PILING DATE: 1999-09-24
PRIOR PILING DATE: 1999-09-24
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 1764
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 532
CURRENT APPLICATION NUMBER: US/10/984,919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1273, Application US/10984919
Publication No. US20050130927A1
GENERAL INFORMATION:
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Publication No. US20040006030A1
GENERAL INFORMATION:
APPLICANT: Stean M. Freier
APPLICANT: Kenneth W. Dobie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTTTCACCAAATTGGAAGC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCTTTCACCAAATTGGAAGC 20
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                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                       TYPE: DNA
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SEQ ID NO 1275 LENGTH: 16

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APPLICANT: Blume, John
TILE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.11
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 862259
LENGTH: 25
                                                                                                                                                                                     Sequence 1215. Application US/10984919

Publication No. US20050130927A1

GENERAL INFORMATION:

APPLICANT: Schlingensiepen, Karl-Hermann

APPLICANT: Schlingensiepen, Karl-Hermann

APPLICANT: Brysch, Wolfgang

TITIE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

FILE REFERENCE: 10496/F63763USO

CURRENT APPLICATION NUMBER: US/10/984,919

FRIOR APPLICATION NUMBER: US/99/341,700

PRIOR APPLICATION NUMBER: PCT/EP98/00497

FRIOR APPLICATION NUMBER: PCT/EP98/00497

FRIOR FILING DATE: 1998-01-30

FRIOR FILING DATE: 1998-01-30

FRIOR PLING DATE: 1998-01-30

FRIOR FILING DATE: 1998-01-30
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OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 16; DB 9; Lot 100.0%; Pred. No. 4.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 862259, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CTTTCACCAAATTGGAAGC 20
                                                                        1 TCACCAAATTGGAAGC 16
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 1764
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1215
LENGTH: 18
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US-11-036-317-862259
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Best Local Similarity
Matches 17; Conserv
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US-11-036-317-862259/c
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APPLICANT: Brysch, Wolfgang
APPLICANT: Schlingensiepen, Rarl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Bogdahn, Ulrich
TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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80.0%; Score 16; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                     DB 9; Length 16;
4.1e+02;
                                                                                                                                                                                                          0; Indels
                                                  CTHER INFORMATION: Description of Artificial Sequence:
CTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/146,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
STREET: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
                                                                                                                                                     Query Match 80.0%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 4.1 Matches 16; Conservative 0; Mismatches
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REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 79, Application US/10146058 Publication No. US20030040499A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLÍCATION DATA:
APPLICATION NUMBER: 08/535,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 79.
ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                          5 TCACCAAATTGGAAGC 20
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LENGTH: 18 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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US-10-146-058-79
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US-11-060-756-239401
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; ORGANISM: probe
US-11-060-756-239401
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                                                TYPE: DNA
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| Sequence 940468, Application US/11036317 |
| Publication No. US20050214823A1 |
| Publication No. US20050214823A1 |
| APPLICANT: Williams, Alan |
| APPLICANT: Williams, John |
| TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse |
| FILE REPERENCE: 3654.1 |
| CURRENT FILING DATE: 2005-01-13 |
| PRIOR APPLICATION NUMBER: US 60/536,639 |
| PRIOR PELLING DATE: 2004-01-13 |
| NUMBER OF SEQ ID NOS: 991174 |
| SEQ ID NOS 40468 |
| LENGTH: 25
               Sequence 873649, Application US/11036317
Sequence 873649, Application US/11036317
CENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Williams, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
: SEQ ID NO 873649
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Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REPERENCE: 3527,1
CURRENT PILING DATE: 2003-11-20
CURRENT PILING DATE: 2003-11-20
PRIOR FILING DATE: 2002 11 20
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
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Matches 17, Conservative
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; ORGANISM: Mus musculus
US-11-036-317-940468
                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Mus musculus US-11-036-317-873649
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US-10-719-956-259831/c
-11-036-317-873649/c
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Sequence 239401, Application US/11060756
Publication No. US2050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
TITLE OF INVENTION: Target Gene
TITLE OF INVENTION: Target Gene
TITLE OF INVENTION: Target Gene
TITLE OF SEQ ID NOS: 3031895-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 233401
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                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FUDICACION NO. USZUUSU130927A1
; GENERAL INFORMATION:
; APPLICANT: SCHLINGENBATION:
; APPLICANT: SCHLINGENBEDEN, KAR1-HERMAIN
; APPLICANT: SCHLINGENBEDEN; MOLÉGANG
; TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763U50
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR PLLING DATE: 1999-02-24
; PRIOR PLLING DATE: 1999-02-24
; PRIOR PLLING DATE: 1999-01-30
; PRIOR PLLING DATE: 1999-01-31
; PRIOR PLLING DATE: 1999-01-31
; NUMBER OF SEQ ID NOS: 1764
; SEQ ID NO 1274
; LENGTH: 15
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                                                                                                                                                                          Score 15.2; DB 7; Length 25; Pred. No. 1.2e+03; 0; Mismatches 3; Indels
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 259831
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 15; DB 9; Le
100.0%; Pred. No. 1.3e+03;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1274, Application US/10984919; Publication No. US20050130927A1
                                                                                                                                                                                                                                                                                   1 GCTTTCACCAAATTGGAAGC 20
                                                                                                                                                                                                                                                                                                                                23 GCTGTCAGCAAATTTGAAGC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                  76.0%;
85.0%;
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                                                                                                        ; ORGANISM: Rattus norvegicus
US-10-719-956-259831
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Best Local Similarity 85.04
Matches 17; Conservative
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US-10-719-900-974400/c
Sequence 974400 Application US/10719900
Publication No. US20050026164A1
GENERAL INPORMATION:
APPLICANT: Xue Mei Zhou
TILLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11.20
PRIOR FILING DATE: 2002 11.20
PRIOR FILING DATE: 2002 11.20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGHH: 25

***CHART SET SECTION NUMBER: MICROARRANTE NUMBER: MIC
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Query Match 74.0%; Score 14.8; DB 10; Length 25; Best Local Similarity 88.9%; Pred. No. 1.9e+03; Matches 16; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-974400
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Search completed: March 4, 2006, 07:04:14 Job time : 419.368 secs

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CQ986684 Sequence
AR455613 Sequence
AX353402 Sequence
AL773120 Arabidops
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PALENL: WO 9425578-A 72 10-NOV-1994;
BIOGNOSTIK GES (DE)
                                                                                  AR110778 Sequence
C2130581 Sequence
BD203423 Method an
AR393715 Sequence
AR647382 Sequence
AR647435 Sequence
AR321595 Sequence
AR321595 Sequence
AR29597 Sequence
BD184058 Method an
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Sequence 72 from Patent WO9425578.
A40535.
A40535.1 GI:2296570
                                              AX008975
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Best Local Similarity 100.
Matches 18; Conservative
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TITLE
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A40535
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A89061 Sequence 12
BD0666574 An antise
BD234905 A method
CS123679 Sequence
AX032815 Sequence
AX030110 Sequence
AX030110 Sequence
AX152494 Sequence
AX11431 Sequence
BD24967 A method
AX009038 Sequence 12
BD066642 An antise
BD066642 An antise
BD066642 An antise
AX08999 Sequence 12
BD066642 An antise
BD066642 An antise
                                                                4, 2006, 01:42:16; Search time 861.632 Seconds (without alignments)
1187.494 Million cell updates/sec
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           5.1.7
Biocceleration Ltd.
                                                                                                                                                                            5883141 segs, 28421725653 residues
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          version 5
- 2006 E
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Maximum Match 100%
Listing first 45 summaries
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AX009038
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Gapop 10.0 , Gapext 1.0
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          GenCore
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PAT 05-MAR-1997

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Result

PAT 22-JAN-2000

98113974.4 PI EN, WOLFGANG PI

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ORIGIN

FEATURES

AUTHORS JOURNAL

REFERENCE

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                             Cases 1 to 18)

Schlingensiepen, K. H., Schlingensiepen, R. and Brysch, W. Schlingensiepen, R. and Brysch, W. Schlingensiepen, R. and Brysch, W. Schlingensiepen, R. and Sytem Stimulating the immune system

Patent: JP 2002517434-A 9 18-JUN-2002;

BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH

SOS Homo sapiens (human)

PN JP 2002517434-A/9

PP 18-JUN-2002

PP 19-JUN-1999 JP 2000553044

PR 10-JUN-1998 EP 98113974.4 P

RARL HERMANN SCHLINGENSIEPEN, REIMAR SCHLINGENSIEPEN, WOLFGANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlingensiepen, K.H.

Combination therapy associating a tgf-beta antagonist with a chemotherapeutic agent and 2005/913-A 30 30-JUN-2005;

Antisense Pharma GmbH (DE)

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        00, A61P95/00,
A61P35/02, A61P37/02, C12N15/09, A61R37/02, C12N15/00 od for stimulating the immune system
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                /organism='Homo sapiens (human)'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 18; DB 6; Length 18; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
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CS123679
CS123679.1 GI:70912172
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CS123679
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SOURCE
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Schlingensiepen, K.H. and Brysch, W.
An antisense oligonucleotide preparation method
Patent: JP 201511000-A 1209 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JULY 2001511000-A/1209
07-AUG-2001
07-AUG-2001
31-0JAN-1999 BP 1998532533
31-0JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N15/11, C7H21/04, AG1K31/70
An antisense oligonucleotide preparation method FH
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches , 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   Length 18;
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  unclassified sequences.

1 (bases 1 to 18)

Brysch, W. and Schlingensiepen, K.

AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

PATENT: WO 9833904-A 1209 06-AUG-1998;

BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)

Location/Qualifiers
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A method for stimulating the immune system.
BD234905.1 GI:33044675
DP 2002517434-A/9.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 18; DB 6; Le Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 18; Conservative 0; Mismatches 0;
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Location/Qualifiers

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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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AUTHORS

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DEFINITION

RESULT 3 BD066574

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PAT 16-JUL-2005

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unclassified sequences.
                Homo sapiens (human)
Homo sapiens
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               PAT 20-DEC-2002
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                      1 (Dases 1 to 18)
Schlingensiepen, G.-F., Brysch, W., Schlingensiepen, K.-H.,
Schlingensiepen, G.-F., Brysch, W., Schlingensiepen, K.-H.,
Antisense-oligonucleotides for transforming growth factor-.beta.
(TGF-.beta.)
(TGF-.beta.)
Batent: US 6455689-A 72 24-SEP-2002;
Biognostik Gesellschaft fur Biomolekulare Diagnostik mbH;
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Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0;
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         18 bp | Sequence 72 from patent US 6455689. AR232815. AR232815.1 GI:27275153

    .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 72 from Patent EP1008649.
AX030110 GI:10190327
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AX008976

    .18
    /organism="unknown"
    /mol_type="genomic DNA"

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Homo sapiens
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Unclassified.
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                                                                                                                   Bogdahn, U., Brysch, W., Schlingensiepen, G.F., Schlingensiepen, K.H. and Schlingensiepen, R.
Antisense-oligonucleotides for the treatment of immuno-suppressive effects of transforming growth factor-b2(tgf-b2)
Patent: EP 100649-A 72 14-JUN-2000;
BIOGNOSTIK GES (DE)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mixture comprising an inhibitor or suppressor of a gene and a molecule binding to an expression product of that gene Patent: WO 0168146-4 20-SEP-2001;
Biognostik Gesellschaft fuer biomelekulare Diagnostik mbH (DE)
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Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 72 from Patent EP1160319.
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Sequence 4 from Patent WO0168146.
AX252494
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PAT 06-SEP-2000

REFERENCE AUTHORS

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Eukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                 Brysch, W., Schlingensiepen, K.H. and Schlingensiepen, R. A method for stimulating the immune system Patent: WO 9963975-A 71 16-DBC-1999, BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE); Location/Qualifiers
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100.0%; Pred. No. 2.6e+02;
Live 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 1277 from Patent WO9833904.
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    .22
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Sequence 71 from Patent WO9963975.
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A61P37/02, A61P37/02, C12N15/09 CC
A61P37/02, A61P37/02, C12N15/09 CC
A61P37/02, 
                        Schlingensiepen, G.F., Brysch, W., Schlingensiepen, K.H., Schlingensiepen, R. and Bogdahn, U. Antisense-Oligonucleotides for the treatment of immunosuppressive effects of transforming growth factor-beta (tgf-beta) Patent: BP 1160319-A 72 05-DEC-2001; BIOGONOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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PN JP 2002517434-A/71
PD 18-JUN-2002
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A method for stimulating the immune system.
BD234967
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JP 2002517434-A/71.
Homo sapiens (human)
Homo sapiens
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REFERENCE AUTHORS

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Schlingensiepen, K.H. and Brysch, W.
An antisense Oligonucleoride preparation method
Patent: JP 201511000-A 1277 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N15/11, C07H21/04, AG1K31/70
An antiesense oligonucleotide preparation method FH
Location/Qualifiers
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unclassified sequences.
1 (Jobb, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLEOTIDE PREPARATION METHOD PALENT, GES (DE) BYSCH WOLFGANG (DE)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.1e+03;
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31-JAN-1997 EP 97101531
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Query Match
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1 CGGCATGTCTATTTTG 16

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Search completed: March 4, 2006, 10:47:50 Job time: 862.632 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21 22 24	c 16 c 17 c 18 c 19		c 10	0 0 4 0 0	Result No.
12 12 11.8 11.8	12.2 12.2 12.2 12.2 12.2	12.2 12.2 12.2 12.2 12.2	12.4 12.4 12.4 12.2	13.8 13.4 13.2 13.2	Score
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Sequence 3, Appli Sequence 65, Appl Sequence 105, App Sequence 631, App	Sequence 134, App Sequence 134, App Sequence 113, App Sequence 113, App Sequence 113, App	Sequence 9, Appli Sequence 11, Appl Sequence 113, App Sequence 134, App Sequence 134, App	35 21 11	Sequence 72, Appl Sequence 29, Appl Sequence 7, Appli Sequence 1903, A Sequence 72258, A Sequence 254, App	Description

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	2, Appli	40, Appl	118257,	118256,	118255,	13, Appl	6, Appli	124, App	10510, A	 Appli 	 Appli 	43, Appl	453, App	132, App	88, Appl	132, App	88, Appl	 Appli 	Appli	61, Appl	. 5182195

ALIGNMENTS

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/535,249 FILING DATE: CLASSIFICATION NUMBER: US/08/535,249 FILING DATE: CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: EP 93 107 089.0 FILING DATE: 30-APR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: EP 93 107 849.7 FILING DATE: 13-MAY-1993 ATTORNEY/AGENT INFORMATION: NAME: Player, William E. REGISTRATION NUMBER: 31,409 REFERENCE/DOCKET NUMBER: 10577/P58418 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 638-666 TELEPHONE: (202) 638-6666 TELEPHONE: (202) 393-5550 TELEPHONE: (202) 393-5550 TELEPHONE: RCA 248593 IDEA UR INFORMATION FOR SEQ ID NO: 72: SEQUENCE CHARACTERISTICS: LENGTH: 18 base pairs TYPE: nucleic acid STRANDEDNESS: unknown	US-08-535-249-72 US-08-535-249-72 US-08-535-249-72 Sequence 72, Application US/08535249 Fatent No. 6455889 GENERAL INFORMATION: APPLICANT: Schlingensiepen, Georg-Ferdinand APPLICANT: Schlingensiepen, Karl-Hermann APPLICANT: Schlingensiepen, Reimar APPLICANT: Schlingensiepen, Reimar APPLICANT: Schlingensiepen, Reimar APPLICANT: Bogdahn, Ulrich APPLICANT: Bogdahn, Ulrich ITITLE OF INVENTION: Amuno-suppressive effect of transforming-growth-factor beta ('UNIMER OF SEQUENCES: 137) CORRESPONDENCE ADDRESS: ADDRESSE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C COUNTRY: U.S.A. ITIP: 2004 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: DC-DOS/MS-DOS OPERATING SYSTEM: DC-DOS/MS-DOS

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RESULT 3
US-10-053-662A-7
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                                                                          ; OTHER INFORMATION: primer US-10-053-662A-7
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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-429-322-29
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GENERAL INFORMATION:
   Query Match 74.7
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                                                                                                                                                                                             TITLE OF INVENTION: ISOLATION OF THE LAMININ Y2 GENE IN
TITLE OF INVENTION: HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS
TITLE OF INVENTION: BULLOSA
FILE REFERENCE: D84us4
CURRENT APPLICATION NUMBER: US/10/053,662A
CURRENT FILLING DATE: 2002-01-24
NUMBER OF SEQ ID NOS: 32
SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Coweert
TITLE OF INVENTION: ANTISENSE MODULATION OF
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-01.00
CURRENT APPLICATION NUMBER: US/09/429,322A
CURRENT FILING DATE: 1999-10-26
CURBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alexandra Charlesworth
APPLICANT: Falvia Spirito
APPLICANT: Guerrino Meneguzzi
APPLICANT: John Baird
APPLICANT: Keith Linder
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TYPE: DNA
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TYPE: DNA
ORGANISM: Artificial Sequence
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MOLECULE TYPE:
ANTI-SENSE: YE
                                                                                                         FEATURE:
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88.2%; Pred. No. 9.7e+02;
7. Mismatches 2;
74.4%; Score 13.4; DB 3; Length 20; 93.3%; Pred. No. 1.6e+03; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 18; DB 3; 100.0%; Pred. No. 7.3;
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                                                                                                                                         US-09-396-196G-72258
                                                                                                                                                                                                                                                                         APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLB OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION UNDER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-396-196G-72258/c
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19083
LENGTH: 25
                                                                                                                                                                                                         PRIOR FILING DATE: 1998-09-17
NUMBER OF SEG ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72258
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 72258, Application US/09396196G Patent No. 6821724 GENERAL INFORMATION:
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                                                                      Matches
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/396,196G CURRENT FILING DATE: 1999-09-15 PRIOR APPLICATION NUMBER: 60/100,678 PRIOR FILING DATE: 1998-09-17
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APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                      TYPE: DNA
ORGANISM: mus musculus
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                                                                                                                                                                                           LENGTH: 25
20
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                                1 CGGCATGTCTATTTTGTA 18
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 CGGCATGTTTAGTTTGAA
                                                                    Conservative
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Pred. No. 26
                                                                                   Score 13.2; DB Pred. No. 2e+03;
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RESULT 6 US-09-526-193A-254/c · Sequence 254, Application US/09526193A

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APPLICANT: Hayden, Michael R.
APPLICANT: Brooks-Wilson, Angela R.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 254
LENGTH: 22
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Best Local :
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PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: 60/138,048
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/139,600
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/393,905
CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: PCT/US01/29340
PRIOR FILING DATE: 2001-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LIBERMANN, TOWIA
APPLICANT: GOLDRING, MARY
TITLE OF INVENTION: USE OF TRANSCRIPTION FACTORS FOR TREATING INFLAMMATION
TITLE OF INVENTION: AND OTHER DISEASES
FILE REFERENCE: 49923CIP (72037)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pimstone, Simon N.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
TITLE OF INVENTION: CHOLESTEROL LEVELS
FILE REFERENCE: 50110/002005
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2,1
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/234,379 PRIOR FILING DATE: 2000-09-20
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CURRENT FILING DATE: 2000-03-15
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                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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ORGANISM: Homo sapiens
                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                      Q ID NO 35
LENGTH: 20
                                                                                            Local
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                                                                         Similarity 92.9
                                  CATGICTATITIGT 17
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  CATGICITITITGT 15
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87.5%;
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Pred. No. 3
                                                                         Score 12.4; DB 3;
Pred. No. 5e+03;
0; Mismatches 1;
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RESULT 8

APPLICANT: Cohen, Daniel APPLICANT: Blumenfeld, Marta APPLICANT: Chumakov, Ilya

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RESULT 10
US-09-422-978-11332/c
Sequence 11332, Application US/09422978
Patent No. 6537751
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SEQ ID NO 21
LENGTH: 20
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 24
   GENERAL
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Patent No. 6563014
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 96700/552
CURRENT APPLICATION NUMBER: US/09/460,555
CURRENT FILING DATE: 1999-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 03988/100K297-US1
CURRENT APPLICATION NUMBER: US/10/660,253
CURRENT FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 60/410,663
PRIOR FILING DATE: 2002-09-12
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TITLE OF INVENTION: METHODS AND SYSTEMS FOR ESTIMATING THE MELTING TEMPERATURE (Tm)
TITLE OF INVENTION: POLYNUCLEOTIDE MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Paul, Jessie B.
TITLE OF INVENTION: SELF-CONTAINED SYSTEM FOR
                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: artificial sequence
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INFORMATION:
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Patent No.
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LENGTH: 18
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 11796
                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/024
FILING DATE: 01-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/843
APPLICATION NUMBER: 07/843
FILING DATE: 28-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer_bind
LOCATION: 1..18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Strom, Terry
APPLICANT: Rubin-Kelly, Vici
APPLICANT: Libermann, Towia
                                                                            NAME: Paul T. Clark, Esq.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 05311/012001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PS/2 Model 50Z or 55S;
OPERATING.SYSTEM: MS-DOS (Version 5
SOFTWARE: WordDerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                           TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/273,402B FILING DATE: 11-JUL-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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5. 5958403
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                                                                                                                                                                                                                                                                                                                                                                                                                IBM PS/2 Model 50Z or 55SX
SYSTEM: MS-DOS (Version 5.0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relly, Vicki E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREVENTION OF GRAFT REJECTION
12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.8%; Score 12.2;
82.4%; Pred. No. 6.
                                                                                                                                                                                                                     07/843,731
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US-09-903-013-11
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                                                                                                                                                                                                                                                                                                           RESULT 13
US-08-823-516-113/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0 SEQ ID NO 11 LENGTH: 25
                                                                                                                                                                                                                                                                              Sequence 113, Application US/08823516 Patent No. 5994069
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Hall, Jeff G.

APPLICANT: Hymichev, Victor I.

APPLICANT: Mast, Andrea L.

APPLICANT: Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Theiss, Gudrun
TITLE OF INVENTION: Use of Strains of Parapoxvirus Ovis for Producing Antiviral Medic
TITLE OF INVENTION: and Medicaments Against Cancer
FILE REFERENCE: LeA 34 376
CURRENT APPLICATION NUMBER: US/09/903,013
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: DE10033582.9
PRIOR APPLICATION NUMBER: DE10122451.6
PRIOR APPLICATION NUMBER: DE10122451.6
PRIOR APPLICATION NUMBER: DE10122451.6
PRIOR FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, St
CITY: San Francisco
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                    STATE:
                                              COUNTRY:
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                                                                 California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlapp, Tobias
Siegling, Angela
Knorr, Andreas
Hirth-Dietrich, Claudia
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                                               United States Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Floppy disk
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                                                                                                                                              Detection Of Nucleic Acids By Multiple
Sequential Invasive Cleavages
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82.4%;
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82.4%;
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Pred. No. 6.3e+03;
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Pred. No. 6.3e+03;
                                                   America
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                                                                                                   Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 25;
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SOFTWARE: PatentIn Rel

OPERATING SYSTEM:

IBM PC compatible

PC-DOS/MS-DOS

Release #1.0, Version #1.30

APPLICATION NUMBER:

24-MAR-1997

US/08/823,516

Matches

Best Local Similarity

82.4%;

Pred. No. 6.4e+03; 0; Mismatches 3

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Indels

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TELEFAX: (415) 397-8338 NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
  NAME/KEY: misc_difference
LOCATION: replace(10, "")
OTHER INFORMATION: /note=
OTHER INFORMATION: position
                                                                                                    NAME/KEY: misc difference
LOCATION: replace(9, "")
OTHER INFORMATION: /note-
OTHER INFORMATION: position
                                                                                                                                                                                                                       LOCATION: replace (6..8, OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_difference
LOCATION: replace(4..5, "")
OTHER INFORMATION: /note= "
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LOCATION: replace(3, "")
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_difference
LOCATION: replace(1..2, "n)
OTHER INFORMATION: /note= "
OTHER INFORMATION: position
                                                                                                                                                                                                        OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/682,853 FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US97/01072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                              misc difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other nucleic acid
/desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                         /note= "The residue at this
position is a 2'deoxythymidine 5'-0-(1-Thiomonophosphate)."
/note= "The position is
                                                                                                                                                                                                  /note= "The residues at these
positions are a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 08/599,491
                                                                                                    position
                                                                                                                                                                                                                                                                                                   positions are a 2'deoxyadenosine 5'-O-(1-Thiomonophosphate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "The residues at these
positions are a 2'deoxycytosi
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                                                                                                /note= "The residue at this position is a 2'deoxyguanos
                                                                                                                                                                                                                                                                                                                          /note= "The residues at these
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  residue at this a 2'deoxycytosine
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  5'-0-(1-Thiomonophosphate)."
                                                                                                  5'-0-(1-Thiomonophosphate)."
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Query Match

67.8%; Score 12.2;

DB 2;

Length 31;

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                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
US 08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 24-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                      NAME/KEY: misc_difference
LOCATION: replace(1..2, "
OTHER INFORMATION: /note=
OTHER INFORMATION: positi
                                                  LOCATION: replace(3, "")
OTHER INFORMATION: /note= "The
OTHER INFORMATION: position is
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                                                                                     NAME/KEY: misc_difference replace(3, "")
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                                                                                                                                                                                                                          DESCRIPTION:
                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ingolia, Diane E
REGISTRATION NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                   NAME/KEY:
                                                                                                                                                                                                                                                                                                            ENGTH:
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San Francisco
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                                                                                                                                                                                                                                                                                                           31 base pairs
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VENTION: Cleavage Of Nucleic Acids
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                                                                                                                                                                                                                                                                                                                                                               (415) 397-8338
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misc_difference
replace(4..5, "")
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0 Montgomery Street,
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                                                                                                                                      positions
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                                                  residue at this a 2'deoxythymidine 5'-O-(1-Thiomonophosphate)."
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                                                                                                                                      2'deoxycytosine
                                                                                                                                      5'-0-(1-Thiomonophosphate)
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US-08-758-314-134/c
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           TELEPHONE: (415) 705-84:
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                APPLICATION NUMBER: US 08/
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
ETITING DATE: 34-TAN 1866
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APPLICANT: Lyamiche
APPLICANT: Lyamiche
TITLE OF INVENTION:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PARTON NUMBER: US 08/
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Improved Cleavage Agents
NUMBER OF SEQUENCES: 134
                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                              FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                       NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FO
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CHARACTERISTICS:
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82.4%;
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positions are a 2'deoxythymidine 5'-0-(1-Thiomonophosphate).
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positions are a 2'deoxyadenosine 5'-0-(1-Thiomonophosphate).
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Pred. No. 6.4e+03;
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Search completed: March Job time: 70.1579 secs
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LOCATION: replace(3, ")
OTHER INFORMATION: /note= "T!
OTHER INFORMATION: position i
FEATURE:
NAME/KEY: misc_difference
LOCATION: replace(4..5, "")
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LOCATION: replace(9, "")
OTHER INFORMATION: /note= "The residue at this
OTHER INFORMATION: position is a 2'decrease."
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LOCATION: replace(1..2, "")
OTHER INFORMATION: /note= "
OTHER INFORMATION: position
FEATURE:
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LOCATION: replace(10, "")
OTHER INFORMATION: /note=
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OTHER INFORMATION: /note= "The residues at these
OTHER INFORMATION: positions are a 2'deoxythymidine 5'-0-(1-Thiomonophosphate)."
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positions are a 2'deoxycytosine 5'-0-(1-Thiomonophosphate)."
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                                                                                                                                                                    Score 12.2; DB 3;
Pred. No. 6.4e+03;
                                                                                                                                                      Mismatches
                                                                                                                                                                                      Length 31;
                                                                                                                                                      Indels
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